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ALIGNMENTS

RESULT 1 Q9LDB6 ID Q9LDB6 Query Match Best Local (Matches Q9LDB6; 01-OCT-2000 01-OCT-2000 PRINTS; PRO0367; ETHRSPELEMNT. PRODOM; PD001423; TF ERF; 1. SMART; SM00380; AP2; 1. DNA-binding. SEQUENCE 203 AA; 22322 MW; SEQUENCE FROM N.A. STRAIN-G.don; TISSUE=Root; MEDLINE=20355201; PubMed=10894776; DOI=10.1126/science.289.5477.2; van der Fits L., Memelink J.; "ORCA3, a jasmonate-responsive transcriptional regulator of plant Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle). Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; asterids; lamiids; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae; 05-JUL-2004 (TrEMBLrel. 27, Las AP2-domain DNA-binding protein. Name=orca3; GO; GO:0005634; C:nucleus; IEA. GO; GO:0003700; F:transcription GO; GO:0006355; P:regulation of EMBL; AJ251250; CAB96900.1; -. EMBL; AJ251249; CAB96899.1; -. primary and secondary metabolism."; Science 289:295-297(2000). Spermatophyta; Magnoliophyta; eudic lamiids; Gentianales; Apocynaceae; HSSP; 080337; 2GCC. TRANSFAC; T04751; -. NCBI_TaxID=4058; Catharanthus [nterPro; 181 121 121 203; 61 61 -1 MSEEIISVSDRFLLSLIEEHLLSDNSDDSSSELTSTEENWEEIFADFLNWSGSEIQKRGS Similarity STTSSSSSSSSSSENSGGRKKRRY 203 KGSRIWLGTYETPEDAALAYDAAAFNMRGAKARLNFPHLIGSNISGPVRVNPRKRFPAEP KGSRIWLGTYETPEDAALAYDAAAFWMRGAKARLWFPHLIGSNISGPVRVWPRKRFPAEP PSSESCOSNSMAESCOEDSVVGTPPEAAAGGGCSKDWNRYKGVRRRPWGKFAAEIRDPKK PSSESCQSNSMAESCQEDSVVGTPPEAAAGGGCSKDWNRYKGVRRRPWGKFAAEIRDPKK MSEEIISVSDRFLLSLIEEHLLSDNSDDSSSELTSTEENWEEIFADFLNWSGSEIQKRGS IPR001471; (TrEMBLrel. 15, 0) (TrEMBLrel. 15, 1 Conservative PRELIMINARY; 100.0%; TF ERF 0; Last sequence update) Last annotation update) Created) Score 1058; DB 2; Pred. No. 3.4e-82; Mismatches 0; PRT; CEE84C274312A601 CRC64; factor activity; IEA. transcription, DNA-dependent; DOI=10.1126/science.289.5477.295; 203 ₽ Indels Length 203; 0 IEA Gaps 120 180 180 120 60 0

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TRANSPAC; T04749; -.

GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription f;
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InterPro; IPR001471; TF ERF;
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DNA-binding.
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OKT-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation protein (EREBP).
Putative ethylene response element binding protein (EREBP).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

lamiids; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae;
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Pred. No. 1.4e-24;
7; Mismatches 35
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transcription, DNA-dependent;
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GO; GO:0003700; F:transcription fac
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InterPro; IPR000977; DNA_ligase.
InterPro; IPR001471; TF_ERF.
PRINTS; PR00367; ETHASSELEMNT.
PRODOm; PD001423; TF_ERF; 1.
SMART; SM00380; APP; 1.
SMART; SM00380; APP; 1.
PROSITE; PS00697; DNA_LIGASE_A1; UN
SEQUENCE 226 AA; 25367 MW; C3F8
                                                                                                                                                                      SEQUENCE FROM N.A.
Rounsley S.D., Lin i
Sykes S.M., Mason T
Venter J.C.;
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MEDLINE=22088475; PubMed=12093376;
Haas B.J., Volfovsky N., Town C.D., Tro
Feldmann K.A., Flavell R.B., White O.,
"Full-length messenger RNA sequences grannotation.";
SEQUENCE FR
Nguyen M.,
                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative ethylene response element binding protein
response element binding protein; EREBP).
                                                                                      Town
                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; endicoryledons; core ev
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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HSSP; O80337; 2GCC.
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                     FROM N.
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                                                              , Kaul S.;
(FEB-2002)
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Pred. No. 1.7e-22;
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1; Mismatches
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vage A.R.,
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  Southwick A.,
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R., Adams
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Matches 69
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=22054140; PubMed=12059106;
MEDLINE=22054140; Puthoff D.P., Hart J.K., Rodermel S.R., Baum T.J.;
Mazarri M., Puthoff D.P., Hart J.K., Rodermel S.R., Baum T.J.;
"Identification and Characterization of a soybean ethylene-responsive element binding protein gene whose mRNA expression changes during soybean cyst nematode infection.";
Mol. Plant Microbe Interact. 15:577-586(2002).

Mol. Plant Microbe Interact. 15:577-586(2002).
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004)
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EMBL; AC03238; AAC31840.1; -.

EMBL; A7072471; AAL66886.1; -.

EMBL; A7072471; AAL66896.1; -.

EMBL; A732508; AAK17157.1; -.

EMBL; A732508; AAK17157.1; -.

EMBL; A7370540; AAK17157.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidieurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine
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PRODOM; PD001423; TF ERF; 1.

SMART; SM00380; AP2; 1.

PROSITE; PS00697; DNA LIGASE A1; UNKNOWN 1.

SEQUENCE 226 AA; 25353 MW; 4B2EF81CDD856987 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=EREBP1;
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Palm C.J., Th
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k A., Karlin-Neumann G., Nguye.....

J., Theologis A., Ecker J., Davis R.W.;

J., Theologis A., Ecker J., Davis R.W.;
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Last sequence update)
Last annotation updat
binding protein 1.
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Best Local (
TRANSPAC: T02653; -.

GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005700; F:transcription f;
GO; GO:0006355; p:regulation of t:
InterPro; IPR001471; TF_ERF.
PRINTS; PR00367; ETHRSDELEMNT.
ProDom; PD001423; TF_ERF; 1.
SMART; SM00380; AP2; 1.
SEQUENCE 236 AA; 26520 MW; 680
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription fa
GO; GO:0006355; P:regulation of tr
InterPro; IPR000977; DNA ligase.
InterPro; IPR000977; DNA Ligase.
InterPro; IPR000471; TF ERF:
PRINTS; PR00367; ETHRSPELEMNT.
PRODOM; PD001423; TF ERF; 1.
SMART; SM00380; AP2; 1.
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Q40476;
01-NOV-1996
                                                                                                                                                                                                                                                               STRAIN-BY4; TISSUE-Leaf; Suzuki N., Ohme-Takagi M., Shinshi H.; Suzuki N., Ohme-Takagi M., Shinshi H.; "Immediate early induction of mRNAs for ethylene-responsive transcription factors in tobacco leaf strips after cutting." Plant J. 15:657-665(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BY4; TISSUE-Leaf;
MEDLINE=95276459; PubMed=7756828;
Ohme-Takagi M., Shinshi H.;
"Ethylene-inducible DNA binding p
                                                                                                                                                                                                   EMBL; D38123; BAA07321.1; -. PIR; T02432; T02432. HSSP; O80337; 2GCC.
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PROSITE; PS00697; DNA_LIGASE_A1;
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=-inducible DNA binding proteins
responsive element.";
11 7:173-182(1995).
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Pred. No. 2
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1B875A6EBZA7D56D
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                                                                                                            factor activity; IEA.
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annotation update)
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edons; core eudicots; aster
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.2e-22;
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           CRC64;
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Best Loc
Matches
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SMART; SM00380; AP2; 1.
SEQUENCE 282 AA; 30011 MW
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GO; G
GO; G
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Submitted (AUG-2002) to the EM
EMBL; AF245119; AAF63205.1; -.
EMBL; AF537265; AAP80810.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUB=Leaf;
Scharte J., Baur B.;
Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mesembryanthemum crystallinum (Common ice plant).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta
Spermatophyta; Magnollophyta; eudicotyledons; core
Caryophyllalas; Aizoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
AP2-related transcription factor (Ethylene responsive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=CDBP; Synonyms=EREB;
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GO:0003700; F:transcription
GO:0006355; F:regulation of
erPro; IPR001471; TF ERF.
NTS; PR00367; ETHRSPELEMNT.
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                                                                                                         AGGEAPVAAAPARGKHYRGVRRRPWGKFAAEIRDPAKNGARVWLGTFETAEDAALAYDRA
                                                                                                                                                                                                                        SEDMVLFGVLRDAVHTGWSPQSGSE-SGSGSPAPVTVKPEPV-----DSPVSSPAPVRV 121
                                                                                                                                                                                                                                                                                      WEBIF----
                                                                                                                                                                                                                                                                                                                                       SDFAVLESIRRHLLEDWDPRAGAPAITTGSGPVYHRNSSFSSLYPCLTDNWGELPLKEDD
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                                                 AFNMRGAKARLNFPHLIGSNISGPVRVNPRKRFPAEPSTTSSSSSSSSSSSENSGGRKK
  AFRMRGSKALLNFPLRVNSGEPDPVRITSKRSSP-
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                                                                                                                                            -GCSKDWNRYKGVRRRPWGKFAAEIRDPKKKGSRIWLGTYETPEDAALAYDAA 143
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                                                                                                                                                                                                                                                                                   -ADFLNW---
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the EMBL/GenBank/DDBJ
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Pred.
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Pred. No. 2
                                                                                                                                                                                                                                                                             -SGSEIQKRGSPSSESCQSNSMAESCQEDSVVGTP-PEAA
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No. 4.
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.9e-22;
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  ERSVSSSSSESASPKR--
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RESULT 9
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Matches 82
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GO; GO:0003700; F:transcription f
GO; GO:006355; P:regulation of t
Interpro; IPR001471; TF ERF.
PRINTS; PR00367; ETHRSPELEMNT.
PRODOm; PD001423; TF ERF; 1.
SMART; SM00380; AP2; 1.
                                                                                                                Q9LW50;
Q9LW50;
01-OCT-2000
01-OCT-2000
SEQUENCE FROM N.A. MEDLINE=20181733; Fujimoto S.Y., Oht
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KITAJIMA S., KOYAMA T., Ohme-Takagi M., Shinshi "Characterization of gene expression of NSERFS, of basic PR genes from Nicotiana sylvestris."; Plant Cell Physiol. 41:817-824(2000).
                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheog
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                    ERF2
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HSSP; O80337; 2GCC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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MEDLINE=20399450; PubMed=10945353;
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                 PubMed=10715325;
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Pred. No. 7.7e-21;
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transcription, DNA-dependent;
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    Ohme-Takagi
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RESULT
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Best Local S
Matches 85
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InterPro; IPRO01471; IF_ERF.
Pfam; PF00847; AP2; ...
PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF_ERF; 1.
SMART; SM00380; AP2; 1.
                     Q8LBU9;
01-OCT-2002
01-OCT-2002
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Ethylene res
Arabidopsis
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or send a
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DNA_BIND
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the European Bioinformatics Institute. There was by non-profit institutions as long a
modified and this statement is not removed.
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-!- FUNCTION: Transcription factor that binds
                                                                                                                                              Q8LBU9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB008104;
EMBL; AB018117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Columbi
MEDLINE=20181125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Contains 1 AP2/ERF domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pathogenesis-related promoter element.
SUBCELLULAR LOCATION: Nuclear (Probable).
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T51989; T51989.
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Nakamura Y., Kaneko T., K
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243 AA;
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                                                                                                                                              PRELIMINARY;
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binding factor 2 (ATE
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                       cress!
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RESULT Q40479
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Matches 85
                                    SEQUENCE FROM N.A.

STRAIN-BY4; TISSUE-Leaf;

STRAIN-BY4; TISSUE-Leaf;

MEDLINE-95276459; pubMed=7756828;

Ohme-Takagi M., Shinshi H.;

"Ethylene-inducible DNA binding pro
ethylene-responsive element.";

plant Cell 7:173-182(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription f
GO; GO:0006355; P:regulation of t
Interpro; IPR001471; TF ERF.
PRINTS; PR00367; ETHRSPELEMNT.
PRODOM; PD001423; TF ERF; 1.
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Q40479;
01-NOV-1996
                                                                                                                                                                                                                        Nicotiana tabacum (Common tobacco).

Bukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; eudicotyledc
lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBL)
01-MAR-2004 (TrEMBL)
Ethylene-responsive
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SEQUENCE
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MEDLINE=22088475; PubMed=12093376;
Haas B.J., Volfovsky N., Town C.D., Tro
Feldmann K.A., Flavell R.B., White O.,
"Full-length messenger RNA sequences gi
                                                                                                                                                                                     NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                             Name=EREBP-2
SEQUENCE FROM N.
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2002)
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080337; 2GCC.

0:0005623
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CE 243 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVRITSKR---SSSSSSSSSSSTSSSEN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVRVNPRKRFPAEPSTTSSSSSSSSSENSGGRKKRR
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                                                                                                                                                                                                                                                                                                                                element
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                                                                                                                                                                                                                                              tobacco).
Streptophyta; Embry
Yta; eudicotyledons;
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Pred. No. 1.4e
29; Mismatches
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                                                                                                                                                                                                                                                                 Embryophyta;
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                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                                                                                core
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                                                                                                                                                                                                                                                                   Tracheophyta;
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                                                                                with
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Best Local (
                                                                                                  Matches
                                                                                                                             Query Match
Best Local S
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                                                                                                                                                                                                                                                                              GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription fa
GO; GO:0006355; F:regulation of t:
InterPro; IPR001471; TF ERF:
PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF ERF; 1.
SMART; SM00380; AP2; 1.
                                                                                                                                                                                                                         ProDom; PD001423
SMART; SM00380; J
NON TER 1
SEQUENCE 203 AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Immediate early induction of max transcription factors in tobacco Plant J. 15:657-665[1998].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDIINE=9839243; PubMed=9725022;

Horvath D.M., Huang D.J., Chua N.H.;

"Four classes of salicylate-induced tobacco g

Mol. Plant Microbe Interact. 11:895-905(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
GO; Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicotiana tabacum (Common tobacco).

Bukaryota; Viridiplantae; Streptophyta; Embry,
Spermatophyta; Magnoliophyta; eudicotyledons;
lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Ethylene response element binding protein 1 (Fragment).
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ProDom; PD001423; TF ERF; 1.
SMART; SM00380; AP2; 1.
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GO; GO:0003700; F:transcription
GO; GO:0006355; P:regulation of
GO; GO:0006357; TF SRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BY4;
Suzuki K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF057373; AAC62619.1; -. HSSP; O80337; 2GCC.
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                                                                                            Similarity
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   -- EENWEE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKAAYRMRGSKALLNFPHRIGLNEPEPVRLTAKRRSP-EP---ASSSISSALENGSPKRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202
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                                                                                                  Conservative
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                                                                                                                                                                                                                            22616 MW;
                                                                                                                                31.4%;
41.8%;
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Score 332.5;
Pred. No. 2.
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Pred. No. 2.4e-20;
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                                                                                                                                                                                                                            F62AB477B0B017DE CRC64;
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transcription, DNA-dependent;
                                                                                                  Mismatches
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                                                                                            2.3e-20;
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edons; core e
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Matches 78
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01-JUN-2003
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Bukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
lamiids; Solanales; Solanaceae; Solanum.
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SMART; SM00380; AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AY192367; AAO34703.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and diverse DNA-binding capacity FEBS Lett. 550:149-154(2003).
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MEDLINE=22816770; PubMed=12935902; DOI

MEDLINE=2816770; PubMed=12935902; DOI

TOURNIET B., Sanchez-Ballesta M.T., Jc

Latche A., Pech J.C., Bouzayen M.;

"New members of the tomato ERF family."
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01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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GO; GO:0003700; F:transcription
GO; GO:0006355; P:regulation of
InterPro; IPR001471; TF_ERF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 26, Last annotation updat
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21; Mismatches
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transcription, DNA-dependent;
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, Jones B., Pesquet E., Regad F.,
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dons; core eudicots; aster
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Best Local S
Matches 73
                                                                                                                                                                                                                                                                                               O8037; O93Z36; Q9SUKI;
30-MAY-2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
Ethylene responsive element binding factor 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF_ERF; 1.
SMART; SM00380; AP2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryv
Spermatophyta; Magnoliophyta; eudicotyledons;
lamiids; Solanales; Solanaceae; Solanum.
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01-NOV-1998 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
MEDLINE=20181733; PubMed=10715325;
Fujimoto S.Y., Ohta M., Usui A., S
                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                        protein)
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EMBO J. 16:3207-3218(1997).
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                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        Name=ERF1; Synonyms=ERF-1; OrderedLocusNames=At4g17500;
ORFNames=DL4785W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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G0:0005334; C:nucleus; IEA.
G0:0003700; F:transcription
G0:000355; P:regulation of
G0:0006355; P:regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              itted (JÜL-1998) to th; U89255; AAC50047.1; T07686; T07686.; O80337; 2GCC.
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Pred. No. 5.
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transcription, DNA-dependent; IEA
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edons; core eudicots; aster
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  Ohme-Takagi M.;
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Writtenscriptional activators or represents of GCC box mediated game at expression, 1,333-404(2000).

RE SEQUENCE PROWN N. A.

RE STRAINSON, COLIMBIA;

REDIANSON, COLIMBIA;

REDIANSON, COLIMBIA;

REDIANSON, COLIMBIA;

REDIANSON, COLIMBIA;

REDIANSON, COLIMBIA;

RESIDENCE PROWN N.

RE STRAINSON, COLIMBIA;

RE STRAINSON,
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MEDLINE=22954650; PubMed=14593172; DOI=10.1126/science.1088305; A Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J., A Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J., A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F., A Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G., A Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J., A Miranda M., Quach H.L., Tripp M., Chang J.M., Akiyama K., Ansari Y., A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P., A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P., A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P., A Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M., A Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M., A Kamiya A., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J., Kawai J., Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T., A Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T., Kawai J., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; "Empirical analysis of transcriptional activity in the Arabidopsis
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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MEDLINE=98409552; PubMed=9736626; DOI=10.1093/emboj/17.18.5484;

Allen M.D., Yamasaki K., Ohme-Takagi M., Tateno M., Suzuki M.;

"A novel mode of DNA recognition by a beta-sheet revealed by the solution structure of the GCC-box binding domain in complex with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a celebrate the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formodified and this statement is not removed.
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"Nuclear events in ethylene signaling: a transcriptional cascade
mediated by ETHYLENE_INSENSITIVE3 and ETHYLENE-RESPONSE-FACTOR1.";
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Science 302:842-846(2003).
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                                                                                                                            Propom; PD001423; TF_ERF; 1.

3D-structure; DNA-binding; Nuclear protein; Transcription
DNA_BIND 143 208 AP2/EDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB008103; BAA32418.1; ALT_INIT.
EMBL; Z97343; CAB45963.1; ALT_FRAME.
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Solano R., Stepanova A.N., Chao Q
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[4]
                                                                                                       SEQUENCE
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ProDom; PD001423; TF_ERF; 1.
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FUNCTION: Transcription factor that binds to the GCC-box pathogenesis-related promoter element.

SUBCELIULAR LOCATION: Nuclear (Probable).

INDUCTION: Ethylene induction of ERF1 is completely dependence of the completely dependence of the completely dependence of the completely dependence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     frameshift in position 44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL161546; CAB78753.1; ALT_FRAME.
AY058174; AAL25588.1; -.
AY062533; AAL32611.1; -.
BT002578; AAO00938.1; -.
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36.0%;
Score 324; DB 1;
Pred. No. 1.7e-19;
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SSNEN-GAPKKRR
                                               FETAEDAALAYDRAAFRMRGSRALLNFPLRVNSGEPDPVRIKSKR
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238
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Search completed: February 27, Job time: 177 secs 2005, 22:06:06

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Maximum Match 100%
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3: geneseqp2000s:*
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(without alignments)
481.671 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	տ	4.	w	N	_	Result No.
336	338	338	338	338	338	338	338	345	356	356	356.5	356.5	356.5	356.5	356.5	356.5	356.5	356.5	357.5	358	358	382	400	1058	Score
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243	244	243	243	243	243	243	243	282	202	202	226	226	226	226	226	226	212	183	183	226	212	210	227	203	Length
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AAG08167	AAG43672	AD003419	AD002257	ADI43611	ABO43109	AAU93144	AAE02522	ADI42040	ADM72375	ADM72373	ADN73807	AD001615	ADI41543	ADE37189	AAE02464	AAG34780	AAG34781	AAG34782	AAG24801	AAG24799	AAG24800	AAY97227	ADG00355	AAY97228	ID
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	0
306	307.5	312	312	312	312	316	319.5	319.5	321.5	321.5	322	324	324	324	324	324	324	324	147
28.9	29.1	29.5	29.5	29.5	29.5	29.9	30.2	30.2	30.4	30.4	30.4	30.6	30.6	30.6	30.6	30.6	30.6	30.6	
303	191	188	188	188	188	250	186	147	187	148	266	268	268	268	268	268	268	268	6
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Aae33251	Adg00356	Adn72841	Aag43437	Aag45284	Aag05108	Aag45283	Aag08168	Aag08169	Aag43673	Aag43674	Aag05107	Ado01625	Adi41547	Ade37257	Abo43101	Adb23098	Aau92963	Aae02506	
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RESULT 1 AAY97228 AAY97228 standard; protein; AAY97228; 203 ₽

ALIGNMENTS

Plant transcription factor AP2 DNA-binding domain polypeptide 19-DEC-2000 (first entry)

AP2; transcription factor; plant metabolism; metabolite; primary; secondary; alkaloid; terpenoid indole alkaloid; TIA; pharmaceutical; food colouring; flavouring; fragrance; antimicrobial; pathogenic; insecticide; gene expression; modulation.

Catharanthus roseus.

WO200046383-A2

10-AUG-2000.

07-FEB-2000; 2000WO-NL000075

05-FEB-1999; 10-FEB-1999; 99DK-00000158. 99US-0119388P.

(UYLE-) RIJKSUNIV LEIDEN.

Memelink J, Van Der Fits CTE, Menke FLH, Kijne JW;

2000-499380/44. DB; AAA53745.

N-PSDB;

Modulating level of metabolites and stress resistance in recombinant cells for synthesis of plant metabolites such as alkaloids including terpenoid indole alkaloids, by providing transcription factor to the cell.

Disclosure; Page 97-98; 101pp; English.

Many plant secondary metabolites have value as pharmaceuticals, food colourings, flavours and fragrances. Some plant secondary metabolites are linked to plant or plant cell defence mechanisms and may confer to the plant antimicrobial activity, protection against UV light, herbivores, pathogens, insects and nematodes. Plant secondary metabolites such as terpenoid indole alkaloids (TIA) represent a class of pharmaceutically useful compounds which naturally occur in many plant species. New methods are described which modulate the expression of one or more genes involved

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Matches 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secondary metabolite modulator; biosynthesis; alkaloid; phenylpropanoid; tobacco; Nicotiana tabacum variant bright yellow; Nicotiana tabacum BY;
                       New isolated polypeptides and polynucleotides useful for biosynthesis of secondary metabolites (e.g. alkaloids or phenylpropanoids) in an organism or its cell.
                                                                                                                                                                                                                                                                                                                                                                                          17-MAY-2002;
04-JUL-2002;
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2002EP-00077674.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AP2; transcription factor; plant metabolism; metabolite; primary; secondary; alkaloid; terpenoid indole alkaloid; TIA; pharmaceutic; food colouring; flavouring; fragrance; antimicrobial; pathogenic; insecticide; gene expression; modulation.
                                                                        Modulating level of metabolites and stress resistance in recombinant cells for synthesis of plant metabolites such as alkaloids including terpenoid indole alkaloids, by providing transcription factor to the
                                                                                                                                                                                                                                                                                                                                                                         05-FEB-1999;
10-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRKRFPAEPSTTSSSSSSSSSENSGGRKKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAEIRDPERRGARLWLGTYETPEDAALAYDQAAFKIRGSRARLNFPHLIGSNIPKPARVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SESCQSNSMAESCQEDSVVGTPPEA-----AAGGGCSKDWNRYKGVRRRPWGKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFSELDFLQSIENHLLNYDSD------FSEIFSPMSSSNALPNSPSSSFGSFPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVSDRFLLSLIEEHLLSDNSDDSSSELTSTEENWEEIFADFLNWS---GSEIQKRGS-PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARRSRTRSPQ-PSSSSCTSSSEN--GTRKRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                     Van
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                                                                                                                                                                                                                                                                     Der Fits
                                                                                                                                                                                                                                                                                                                         LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
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44.1%;
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Pred. No. le-34;
2; Mismatches
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                                                                                                                                                                                                                                                                     FLH,
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                                                                                                                                                                                                                                                                     Kijne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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Disclosure; Page

97;

101pp; English

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RESULT 4
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XX AAG2
XX Arab
DT 17-C
XX Arab
XX Prot
KW Prot
KW term
XX Arab
XX EP1C
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XX EP1C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC Many plant secondary metabolites have value as pharmaceuticals, food CC colourings, flavours and fragrances. Some plant secondary metabolites are CC linked to plant or plant cell defence mechanisms and may confer to the CC plant antimicrobial activity, protection against UV light, herbivores, CC plant antimicrobial activity, protection against UV light, herbivores, CC pathogens, insects and nematodes. Plant secondary metabolites such as CC terpenoid indole alkaloids (TIA) represent a class of pharmaceutically CC useful compounds which meturally occur in many plant species. New methods in the biosynthesis of plant metabolites or their precursors in plant CC cells. The method comprises inserting into a plant cell a sequence CC encoding a transcription factor comprising an AP2 DNA-binding domain and by modifying the expression of that transcription factor. Transcription factors comprising an AP2 DNA-binding domain are useful as central CC regulators of complex metabolite pathways involving numerous target genes for such transcription factors. This means that the yield of commercially CC valuable metabolite compounds can be enhanced and the tolerance of plants CC towards exogenous stress factors can be influenced. The method is useful CC for modulating the level of one or more metabolite. By providing a CC transcription factor to the cell the level of the metabolite is enhanced CC by at least 10%, 25% or 100% or reduced 10%, 25%, 50% or 90% relative to CC a cell to which the transcription factor is not provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 88
  25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
                                                                                                                                                                                                                                                   Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 28612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                              25-FEB-2000;
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                                                                                                                                                                                                                                                                                            sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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ilarity 43.6%;
Conservative 2
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    99US-0121825P.
99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126264P.
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Pred. No. 8.2e
27; Mismatches
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3.2e-33;
mes 35;
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14-MAY 1999
11-JUN 1999
11-JUN
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99US-01274823P

99US-0128714P

99US-0130449P

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99US-0140823P

99US-0140823P

99US-0142839P

99US-0142803P

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99US-0142803P

99US-0143624P

99US-0143624P

99US-0143624P

99US-0144005P

99US-0144005P
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RESULT 5
AAG24799
ID AAG2
AAG24799
ID AAG2
XX AAG2
XX AAG2
XX AAG2
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EN Prot
KW Prot
KW Lern
XX Prot
XX Prot
XX 25-F
PR 25-F
PR 25-F
PR 23-F
PR 09-M
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Matches
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25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
                                                                                     EP1033405-A2
                                                                                                       Arabidopsis thaliana.
                                                                                                                        Protein identification; signal transduction hybridisation assay; genetic mapping; gene etermination sequence.
                                                                                                                                                               Arabidopsis thaliana protein fragment
                                               25-FEB-2000;
                                                                  06-SEP-2000.
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                                                                                                                                                                                                                                                                                           139
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                                                                                                                                                                                                                                                                                                                                                                                          79;
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                VGTPPEAAAGGGCS--KDWNRYKGVRRRPWGKFAAEIRDPKKKGSRIWLGTYETPEDAAL
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                                                                                                                                                                                                                                                                                                                                                    ILNDNWSDLPLSVDDSQD-----MAIYNTLRDAVSSAWTPSVPPVTS-----PAEEDK-
                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                              PPATKASGSHAPRQKGMQYRGVRRPWGKFAAEIRDPKKNGARVWLGTYETPEDAAV
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                                                2000EP-00301439
                                                                                                                                                                                    (first
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99US-0123180P.
99US-0123548P.
99US-0125788P.
                                                                                                                                                                                                                        protein; 226
                                                                                                                                                                                                                                                                                                                                                                                                  33.8%;
                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                                                                                                                                                                                                                                                                                        Score 358; DB
Pred. No. 3.4e
24; Mismatches
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                                                                                                                                                                 SEQ ID
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}.4e-30;
nes 55;
                                                                                                                                   n pathway; metabolic
expression control;
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                                                                                                                                                                 28611.
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                                                                                                                                   pathway;
promoter;
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                           194
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24; Mismatches
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25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
23-MAR-1999;
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                                                                                                                                   Arabidopsis thaliana.
                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 42376.
                                                                                                                                                                                                                                                  AAG34781;
                                                                                                                                                                                                                                                                        AAG34781 standard;
                                                                  25-FEB-2000;
                                                                                         06-SEP-2000.
                                                                                                                                                          termination
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120 RAAFQLRGSKAKLNFPHLIGSCKYEPVRIRPRRRSP-EPSVSDQLTSEQKRES 171
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Similarity 61.1%;
69; Conservative 1
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RESULT 10
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Best Loc
Matches
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18-0CT-1999
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14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
                                                                                                                                                                                                                                                                                                                      Key
Domain
                    (MEND-)
                                                                                                 17-APR-2000;
22-AUG-2000;
                                                                                                                                        17-NOV-1999;
                                                                                                                                                                               14-NOV-2000; 2000WO-US031458
                                                                                                                                                                                                                       25-MAY-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                       plant
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                                                                                                                                                                                                                                                            WO200136598-A1
    (CREE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                       structure; plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74
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MENDEL BIOTECHNOLOGY INC PINEDA O.
YU G.
CREELMAN R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPATKASGSHAPRQKGMQYRGVRRPWGKFAAEIRDPKKNGARVWLGTYETPEDAAVAYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPEAAAGGGCS--KDWNRYKGVRRRPWGKFAAEIRDPKKKGSRIWLGTYETPEDAALAYD
                                                                                                                                                                                                                                                                                                                                                                                  thaliana.
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2000US-0227439P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            factor;
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99US-0159584P

99US-0160741P

99US-0160767P

99US-0160776P

99US-0160814P

99US-0160815P

99US-0160981P

99US-0160981P

99US-0161405P

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99US-0161361P

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S066
S066
                                                                                                                                        99US-0166228P.
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3-0159329P.
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61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          environmental
                                                                                                                                                                                                                                                                                                                                                                                                                         development.
                                                                                                                                                                                                                                                                                                     "Conserved domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226
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Pred. No. 5.5e
L5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       æ
                                                                                                                                                                                                                                                                                                                                                                                                                                          stress tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .5e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy;
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RESULT 11
ADE37189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor. This movel transcription factor is useful for modifying a plant's compensation desirable ways, such as modifying a plants environmental stress. The transcription factor is encoded by environmental stress colerance gene derived from Arabidopsis thaliana. The transcription factors and the genes encoding them are used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, canliflower, coffee, onlon, cucumber, eggplant, grapes, honey dew, calliflower, coffee, onlon, cucumber, eggplant, grapes, honey dew, coulting, melon, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas. These sequences are also used for modifying traits associated with environmental stress tolerance, such as freezing, chilling, heat, drought, water saturation, salt, photoconditions, cradiation and ozone. The transcription factors are used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 69
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Reuber
                                                                                                                            microbial disease; fundherbicide sensitivity; growth improvement; ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RIEC/)
(HEAR/)
(RATC/)
(REUB/)
                                                                                                                                                                                                                                                                    ADE37189;
                                                                                                                                                                                                                                                                                                ADE37189 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 226 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present amino acid sequence is Arabidopsis thaliana transcription factor. This novel transcription factor is useful for modifying a plant's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 55-56; 116pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding plant transcription factor polypeptides, for altering the environmental stress tolerance characteristics
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                                                                                                                                                                            transcription factor; tolerance;
                                                                                                                                                                                                        Plant yield
                                                                                                                                                                                                                                        29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEARD J
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Keddie
                                                                                                                                                                                                        related
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                                                                                                                                               fungal dis
ity; heavy
                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                       protein from
                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.7%;
                                                                                                                                                              disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
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                                                                                                                                                                                                                                                                                                   226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 356.5; DB 4;
Pred. No. 5.5e-30;
5; Mismatches 26;
                                                                                                                              nce; environmental condition;
sease; viral disease; pest infestation;
metal tolerance; heavy metal uptake;
dition; nutrient uptake; hormone sensit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Riechmann
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                                                                                                                                                                                                          clone G22.
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of
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09-AUG-2002; 2002WO-US026966.

20-FEB-2003 WO2003014327-A2 Arabidopsis thaliana. transgenic

plant.

photocondition;

sensitivity;

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RESULT 12
ADI41543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a number of cDNA sequence and their encoded proteins which are especially transcription factor cDNAs and their proteins. The isolated or recombinant polynucleotide is useful for proteining a modified plant with a modified trait, e.g. enhanced tolerance to environmental conditions, improved tolerance to microbial, fungal or viral diseases, improved tolerance to pest infestation, decreased herbicide sensitivity, improved tolerance of heavy metals, or enhanced ability to take up heavy metals, improved growth under poor photoconditions, improved nutrient uptake, or reduced hormone sensitivity. The transgenic plants are useful for growing a progeny plant comprising the desired trait. The polynucleotides and polypeptides are also useful in bioinformatic search methods. This sequence represents one of the proteins of the invention.
                                                                   glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; flowering; flower structure; stem bifurcation; branching pattern; apical dominance; trichome; stem morphology; root growth; root hair; seed development; cell proliferation; cell differentiation; premature senescence; necrosts; plant size; leaf morphology; seed morphology; seed biochemistry; root anthocyanin; plant anthocyanin; light response; shade avoidance; bioinformatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001;
19-NOV-2001;
11-DEC-2001;
14-JUN-2002;
                                                                                                                                                                                                         Plant
US2004019927-A1
                            Arabidopsis thaliana
                                                                                                                                                                             transgenic;
                                                                                                                                                                                                                                        22-APR-2004
                                                                                                                                                                                                                                                                                                 ADI41543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MEND-) MENDEL BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stress-related transcription factor polynucleotides and polypeptides, ful for producing transgenic plants with e.g. improved tolerance to eases or pests, decreased herbicide sensitivity, or improved nutrient
                                                                                                                                                                                                                                                                                                                                                                                                      142
                                                                                                                                                                                                                                                                                                                                                                             134
                                                                                                                                                                                                         transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                     74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                      AAAFNMRGAKARLNFPHLIGSNISGPVRVNPRKRFPAEPSTTSSSSSSSSSSEN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPEAAAGGGCS--KDWNRYKGVRRRPWGKFAAEIRDPKKKGSRIWLGTYETPEDAALAYD 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 AA;
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                                                                                                                                                                           plant; enhanced tolerance to abiotic stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID
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2001US-0336049P.
2001US-0338692P.
2002US-00171468.
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                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                  protein;
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u GL, Bro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 356.5; DB 7
Pred. No. 5.5e-30;
5; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Broun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jiang
m PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                             The invention describes a transgenic plant comprising a recombinant comply production of any one of more than 500 nucleotide sequences fully confidence in the specification or its complement. The method of the convention can be used to produced a plant having altered traits such as: consitivity; disease resistance; sugar sensing; early or late flowering; considered flower structure, change in stem bifurcations, altered branching pattern, reduced apical dominance, reduced trichome density; lack of contributions; reduced ectopic trichome development; altered branching trichomes; reduced ectopic trichome number; altered stem morphology; concreased root growth; increased root hairs; altered seed development; considered ell proliferation or cell differentiation; rapid development; considered cell proliferation or cell differentiation; rapid development; considered plant size; leaf morphology; seed morphology; seed biochemistry; increase in root anthocyanins; increase in plant containts, or alteration in light response or shade avoidance. The containts cearch methods. This is the anino acid sequence of a plant transcription factor that can be used in the creation of a transgenic containt with altered traits.
                                                                                                     Matches
                                                                                                                               Query Match
                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New transgenic plant comprising a recombinant of more than 500 nucleotide sequences, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-132245/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pilgrim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Creelman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ADAM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CREE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHER/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-2003; 2003US-00374780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BROU,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JIAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DUBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PILG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAAK/)
                                                                                                                   Local
                                                    74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AN
AN
AN
AN
                                                                                                      69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RATCLIFFE O.
ADAM L J.
REUBER T L.
KEDDIE J.
BROUN P E.
BILGRIM M L.
DUBELL A N.
PINEDA O.
YU G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JIANG C.
HEARD J E.
HAAKE V.
CREELMAN R A.
                                                                                                                   Similarity
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                                                                                                                                                           226
RAAFQLRGSKAKLNFPHLIGSCKYEPVRIRPRRRSP-
             AAAFNMRGAKARLNFPHLIGSNISGPVRVNPRKRFPAEPSTTSSSSSSSSSEN
                                                  Conservative
                                                                                                                                                          Ä
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Ratcliffe O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ħ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; 435pp; English.
                                                                                                                 33.7%;
61.1%;
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                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jiang C,
Adam LJ,
                                                                                                    Score 356.5; DB 8
Pred. No. 5.5e-30;
5; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Reuber
Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heard JE,
Reuber TL,
                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polynucleotide of any
in bioinformatic searc
EPSVSDQLTSEQKRES
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                                                                                                      Indels
                                                                                                                               Length
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                                                                                                                               226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Broun
                          194
 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             search
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Œ;
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ADO01615 standard; protein;

226 AA.

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ADOO1615
ADOO1615
ADOO1615
AC ADOO
AC 
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06-APR-2000;
16-NOV-2000;
27-MAR-2001;
17-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-1999;
21-JAN-2000;
17-FEB-2000;
22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
                                                           Pilgrim
Sherman
WPI; 2004-225755/21.
N-PSDB; ADO01614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-
17-DEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             trichome development; seed development; premature senescence;
delayed senescence; lethality; necrosis; plant size; leaf morphology;
seed morphology; secondary metabolism; light response; shade avoidance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thalecress; transcription factor; plant; transgenic; abiotic str
cold tolerance; heat tolerance; drought; osmotic stress;
phosphate limitation; potassim limitation; nitrogen limitation;
hormone sensitivity; disease resistance; sugar sensing; seed ger
flowering; inflorescence architectural change;
meristem cell differentiation; phyllotaxy; apical dominance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUN-2002;
09-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAR-2004
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                                                                                                                                                                                                                                             (JIAN/)
(SAMA/)
(PILG/)
(CREE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ZHAN/)
(FROM/)
(HEAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-APR-2003; 2003US-00412699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2004045049-A1
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                                                                                                                                                                                                      (DUBE/)
                                                                                                                                                                                                                                                                                                                               (YUGG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                   (RIEC/)
(ADAM/)
                                                                                                                                                                (SHER/)
                                                                                                                                                                                                                                                                                                                                                                                          (PINE/
                                                                                                                                                                                                                                                                                                                                                                       (REUB/)
                                                    1 J,
1 O,
m ML,
1 BK;
                                                                                                                                                                                                FROMM M E.
HEARD J E.
RIECHMANN J L.
ADAM L J.
BROUN P E.
PINEDA O.
REUBER T L.
KEDDIE J S.
YU G.
JIANG C.
SAMAHA R S.
PILGRIM M L.
CREELMAN M L.
CREELMAN R A.
DUBELL A N.
DUBELL A N.
DUBELL FEE O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZHANG
FROMM
HEARD
                                                                                                                                                              KUMIMOTO R. SHERMAN B K.
                                                                                                   Fromm ME
Reuber
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-00489376
2000US-00532591
2000US-005330291
2000US-00533030
2000US-00533392
2000US-00533392
2000US-00533392
2000US-00533492
2000US-00534648
2000US-007109444
2001US-00819142
2001US-00819142
2001US-00819142
2001US-00819142
2001US-00819142
2001US-00819142
2001US-00819142
2002US-00171468
2002US-00225066
2002US-00225066
2002US-00225066
2002US-002374780
                                                                                Creelman
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                                                                                    a ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-00394519
                                                                                                   Heard JE,
Keddie J
                                                                                RΑ,
                                                                              JE, Riechmann JL, Ao
die JS, Yu G, Jiang (
Dubell AN, Ratcliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #14.
                                                                     7 C,
                                                                                                                      Adam LJ,
                                                                                                   Samaha
                                                                              Kumimoto R;
                                                                                                                      Broun PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   germination;
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New transgenic plant, useful in developing improved characteristics or traits. phenotypes with altered

Claim 1; SEQ ID NO 28; 213pp; English

Constitutive, inducible or tissue-specific promoter and a recombinant constitutive, inducible or tissue-specific promoter and a recombinant complynucleotide described above), a bost cell comprising the expression cassette, producing a modified that having a modified that it, identifying a factor that is modulated by or interacts with a polypeptide encoded by the polynucleotide sequence that is subject to a regulatory effect of any of the polynucleotide sequence and identifying at least one downstream polynucleotide sequence that is subject to a regulatory effect of any of the polynucleotide described above. The transgenic plant is useful for producing a plant that has an altered trait, e.g. an enhanced to learance to about stress (increased tolerance to chilling, germination in cold conditions, freezing tolerance to to heat, tolerance to phosphate limitation, tolerance to somotic stress, tolerance to salt, colerance to otherance, discred susceptibility to selection tolerance and the sending of the polynucleotide described above. The crapme to ethylene, disease resistance, altered susceptibility to susceptibility to part of the polynucleotide sending the period of flowering, an inflorescence architectural clange, a change in the middle seed germination and seedling vigor, early flowering, late flowering, axended germination and seedling vigor, early flowering, late flowering, axended germination and seedling vigor, early flowering, late flowering, axended germination and seedling vigor, early flowering, late flowering, axended germination and seedling vigor, early flowering, late flowering, axended germination and seedling vigor, early flowering, late flowering, axended germination and seedling vigor, early flowering, late flowering, axended general flowering, attered seed derelopment, increased lateration, premature sensescence, delayed to stem blight to flowering, an increased necrosis, an increase in seed dividual seed of producing and seed sort in seed in school and seed size, clange in seed seed sortent, ch sequence comprising a sequence encoding a polypeptide, that initiates transcription (i.e. a transcription factor) from Arabidopsis, Soybean, Rice, Rape or Corn, comprising any of the sequences appearing as ADO01588 -ADO03527 or ADO03530-ADO03559. Also included are using a transgenic Sequence 226 light The thalecress transcription polynucleotide having response B relates yanins, increase in plant anthocyanins, or shade avoidance. The present sequencescription factor of the invention. a polynucleotide sequence or to a transgenic plant comprises quence or its complementary polypeptide, that initiate polypeptide, that initiaters) from Arabidopsis, Soybean sequence represents a recombinant

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                                                                             Matches
                                                                                      Query Match
Best Local
                                                                                     Local
134
           142 AAAFNMRGAKARLNFPHLIGSNISGPVRVNPRKRFPAEPSTTSSSSSSSSEN
                                      74
                                                         84
                                                                             69;
                                                                                      Similarity
                                                   PPEAAAGGGCS--KDWNRYKGVRRRPWGKFAAEIRDPKKKGSRIWLGTYETPEDAALAYD
                                       PPATKASGSHAPRQKGMQYRGVRRRPWGKFAAEIRDPKKNGARVWLGTYETPEDAAVAYD
                                                                             Conservative
                                                                                     33.7%;
                                                                            15;
                                                                           Pred. No. 5.5e
5; Mismatches
                                                                                               Score
                                                                                       356.5;
No. 5.
                                                                                       .5e-30
                                                                                                BB
                                                                             26;
                                                                                               8
                                                                             Indels
                                                                                             Length
                                                                                                226;
                                                                            3
                   194
                                                                             Gaps
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ADN73807
XX
AC ADN7
XX
AC ADN7
XX
Thal
DX Thal
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Thal
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Thal
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Thal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up common to a common the common terms of t
                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Altering plant characteristics, useful for producing plants for enzyme pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1702; 134pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-OCT-2002; 2002EP-00079408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-OCT-2003; 2003WO-EP011658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nitrogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2004-348466/32.
   134
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                                                                                                                                                                                                                                                                                                 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transgenic; E2Fa/DPa transcription factor; growth regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CROPDESIGN NV
                                                                                                                                                                                                                                                                                                                                                                                                                                             226
RAAFQLRGSKAKLNFPHLIGSCKYEPVRIRPRRRSP-EPSVSDQLTSEQKRES 185
                                                                                                                                                                                       PPEAAAGGGCS--KDWNRYKGVRRRPWGKFAAEIRDPKKKGSRIWIGTYETPEDAALAYD 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        De
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metabolism; carbon metabolism
                                                                      AAAFNMRGAKARLNFPHLIGSNISGPVRVNPRKRFPAEPSTTSSSSSSSSSSEN 194
                                                                                                                                                PPATKASGSHAPRQKGMQYRGVRRRPWGKFAAEIRDPKKNGARVWLGTYETPEDAAVAYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Veylder L,
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                                                                                                                                                                                                                                                                                                                        33.7%;
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                                                                                                                                                                                                                                                                                             15,
                                                                                                                                                                                                                                                                                         Score 356.5; DB 8;
Pred. No. 5.5e-30;
5; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wall biosynthesis;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                               226;
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                                                                                                                                                                                                                                                                                         Gaps
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RESULT 15
ADM72373
ID M72373
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XX ADM72
XX ADM72
XX CDPK,
XW Plant
KW CDPK,
KW nemat
XX 70M;
KW nemat
XX 61yci
PN W0200
XX 908-AI
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to pathogen-responsive genes that encode a nematode regulated polypeptides. The proteins of the invention include calcium dependent protein kinase (CDPK), nematode-responsive transcription factor 1 (NRTF1), nematode-responsive protein (NRP), caffeic acid 7-0-methyltransferase (70M) or inositol 5-phosphatase (IPP) polypeptides. The nucleic acid molecule encoding the polypeptides are operably linked to a promoter that drives expression in a host cell. The composition and methods are useful for conferring or improving nematode resistance in plants. The present sequence represents a soybean NRTF1c polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic proteins, useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 26; SEQ ID NO 11; 143pp;
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Job time : 165 весв

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343	328	328	251	336	245	222	185	262	303	225	192	263	196	171	295
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T05607	G84826	G86263	T01986	E84594	E86168	T52019	D96572	E96747	T04541	T02433	D96498	T49870	G85435	T00432	T00399
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## ALIGNMENTS

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A;Cross-references: UNIPROT:022167; EMBL:AC002388; NID:g3420042; PID:g2344900
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 199
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
ethylene-responsive transcription factor ERF1 - common tobacco c;Species: Nicotiana tabacum (common tobacco) C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004 C;Accession: T02412 R;Ohme-Takagi, M.; Shinshi, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T00409; D84883 R;Rounds, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mas submitted y S.D.; Lin, X.; Ketchum, K.A.; D97 submitted to the EMBL Data Library, July 1997 A;Description: Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence.
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C;Genetics
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A;Molecule type: DNA
A;Residues: 1-226 <ST
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A; Residues: 1-226 < R
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                                                                                                                                                                                                                                                                                                       142 AAAFNMRGAKARLNFPHLIGSNISGPVRVNPRKRFPAEPSTTSSSSSSSSEN
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ilarity 61.1%;
Conservative 1
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Pred. No. 9.6e-24;
.5; Mismatches 26;
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Plant Cell 7, 173-182, 1995
A;Title: Ethylene-inducible DNA binding proteins that interact with an ethylene A;Title: Ethylene-inducible DNA binding proteins that interact with an ethylene A;Reference number: Z14671; MUID:95276459; PMID:7756828
A;Accession: T02432
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule typ
DNA binding protein EREBP-2 - common to C;Species: Nicotiana tabacum (common to C;Date: 05-Mar-1999 #sequence_revision C;Accession: T02590 R;Ohme-Takagi, M.; Shinshi, H.
                                                                                                                                                      RESULT
T02590
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R;Fujimoto, S.Y.; Ohta, M.; Usui, A.; Shinshi, H.; Ohme-T
Plant Cell 12, 393-404, 2000
A;Title: Arabidopsis ethylene responsive element binding
A;Reference number: Z25893
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A; Status: preliminary; translated
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Pred. No. 4.3e-22;
0; Mismatches 69
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                                                       #text_change
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C;Accession: T51988
R;Fujimoto, S.Y.; Ohta, M.; Usui, A.;
Plant Cell 12, 393-404, 2000
A;Title: Arabidopsis ethylene responsi

A; Reference number:

ethylene Z25893

responsive

element binding factors act

as

transcriptional

Shinshi, H.; Ohme-Takagi,

ethylene responsive element binding factor 1 [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000

RESULT

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C;Species: Lycopersicon esculentum (tomato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999
C;Accession: T07686
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                                                                                                                                                                                                                                                             A;Description: transcription factor A;Note: binds the GCC box, present in t C;Keywords: DNA binding; transcription
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submitted to the EMBL Data
A; Reference number: Z16094
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A;Title: Ethylene-inducible
A;Reference number: Z14671;
A;Accession: T02590
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A; Residues: 1-233 < OHM >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                    C; Function:
                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:004680; EMBL:U89255; NID:g3342210; PIDN:AAC50047.1;
                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-234 < ZHO>
                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: T07686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67;
                               168
                                                                                                 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 VGTPPEAAAGGGCSKDWNRYKGVRRRPWGKFAAEIRDPKKKGSRIWLGTYETPEDAALAY 140
                                                                                                                                65
                                                                                                                                                               49
                                                                                                                                                                                                h 31.0%; Score 328.5; DB 2
Similarity 47.1%; Pred. No. 2.8e-21;
73; Conservative 18; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                 WGKFAAEIRDPKKKGSRIWLGTYETPEDAALAYDAAAFNMRGAKARLNFPHLIGSNISGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RK 197
                                                                                                                                                               NWSGSEIQKRGSPSSESCQSNSMAESCQEDSVVGTPPEAAAGGGCSKDWNR-YKGVRRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RR 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKAAYRMRGSKALLNFPHRIGLNEPEPVRLTAKRRSP-EP---ASSSISSALENGSPKRR
                                                                                                                                  NFTAGEV--KSEPREE-----IESSPEFS--PSPAETTAAPAAETPKGRHYRGVRQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAPPAETTTAQAVVPKGRHYRGVRQRPWGKFAAEIRDPAKNGARVWLGTYETAEEAALAY
                               VRVNPRKRFPAEPSTTSSSSSSSSSSENSGGRKKRR
                                                                WGKFAAEIRDPAKNGARVWLGTYETAEEAAIAYDKAAYRMRGSKAHLNFPHRIGLNEPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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54.9%;
                                                                                                                                                                                                                                                                                  present in the promoter region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 333;
Pred. No. 1
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 -ASSSGNGSMKRRR
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                                                                                                                                                                                                                                                                                of genes
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                                                                                                 167
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                                                                                                                                                                                                                                                                                   pathogenesis
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                                                                                                                                                                                                                                                                                                                                    PID:g334
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RESULT 7

A85,196

EREBP-2 protein [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001

C;Accession: A85,196

R; antonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold

Nature 402, 769-777, 1999

A;Tille: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A;Reference number: A85,001; MUID:20083488; PMID:10617198

A;Accession: A85,196

A;Status: preliminary

A;Rosidues: 1-25 <5TO>

A;Cross-references: GB:NC_001268; NID:g5281024; PIDN:CAB45963.1; GSPDB:GN00140

C;Genetics:
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A;Status: prellminary; translated fro A;Wolecule type; mRNA
A;Residues: 1-266 <FUJ>
A;Cross-references: EMBL:AB008103; P: C;Genetics: A;Grene: ERF-1
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A;Map
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RESULT 8
B86197
hypothetical protein [imported]
hypotheses: Arabidopsis thaliana
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Best Local S
Matches 75
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Best Local S
Matches 89
                                                                                                                                                                                                                                                                                                                                                                                                ;Genetics:
;Gene: dl4785w
                                                                                                                                                                                                                                                                                                                                                                               position: 4
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                                                                                                                                                                                                                                                                          23 SDNSDDSSSELTSTEENWEEIFADFLNWSGSEIQKRGSPSSESCQSNSMAESCQEDSVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
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                                                                                                                                                                                                        TPPEAAAGGGCSKDWNRYKGVRRRPWGKFAAEIRDPKKKGSRIWLGTYETPEDAALAYDA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEDSVVGTPPEAAAGGGCSKDWNRYKGVRRRPWGKFAAEIRDPKKKGSRIWLGTYETPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVSDRFLLSLIEEHLLSDN----SDDSSSELTST-----EE
                                                                                                                                    AAFNMRGAKARLNFPHLIGSNISGPVRVNPRKRFPAEPSTTSSSSSSSSSSSENSGGRKKRR 202
                                                                                                                                                                                                                                          SSSSDEDRSSFPSVKIETPESFA-------AVDSVPVKKEKTSPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAPKKRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AALAYDRAAFRMRGSRALLNFPLRVNSGEPDPVRIKSKR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AALAYDAAAFNMRGAKARLNFPHLIGSNISGPVRVNPRKRFPAEPSTTSSSSSSSSSENS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVKKEKTSPVSAAVTAAKGK---HYRGVRQRPWGKFAAEIRDPAKNGARVWLGTFETAED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NW-----EEIFADFL-----NW----SGSEIQKRGSPS--SESCQSNSMAESC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQSDYAFLESIRRHLLGESEPILSESTASSVTQSCVTGQSIKPVYGRNPSFSKLYPCFTE
                                                                                                      AAFRMRGSRALLNFPLRVNSGEPDPVRIKSKR
                                                                                                                                                                                                                                                                                                           29.5%;
ilarity 41.7%;
Conservative 1
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                                                                                                                                                                                                                                                                                                            19; Mismatches
 - Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                         Score 312; DB 2;
Pred. No. 7.2e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 322; DB 2;
Pred. No. 1.2e-20;
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                                                                                                                                                                                                                                                                                                            46;
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A;Status; procedure type: DNA
A;Molecule type: DNA
A;Residues: 1-207 <BEV>
A;Residues: 1-207 <BEV>
A;Cross-references: UNIPROT:Q9LY05; EMBL;AL163912; GSPDB:GN00063; ATSP:T2I1.290
A;Cross-rimental source: cultivar Columbia; BAC clone T2I1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
T49897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A,Recession: B86197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: T49897
R;Bevan, M.; Murphy, G.;
submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription factor-like protein - Arabidopsis thaliana
N;Alternate names: protein T2I1.290
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
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A; Map position:
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A; Accession: T49897
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문
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A; Residues: 1-244 <STO>
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                                                                                                                                                                                                                                                                Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 AYDAAAFNMRGAKARLNFP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 ENSSSSWSSQESPLWEE---SFLHQSPDQSPLLSSPTDNYCDDFFAFESSIIKEEGKEA
79
                                    52 GSEIQKRGSPSSESCQSNSMAESCQEDSVVGTPPEAAAGGGCSKDWNRYKGVRRRPWGKF 111
                                                                               19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 TVAAEEEEKS-----YRGVRKRPWGKFAAEIRDSTRKGIRVWLGTFDTAEAAAL
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                                                                                                                      4 EIISVSDRFL------LSLIEEHLLSDNSDDSSSELTSTEENWEEIFADFLNWS
                                                                                                                                                                 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
72; Conserv
                                                                                                                                                                                Similarity
SPELNS-SSSTYETDQSVKKAERFEEE
                                                                             EDILIVEDGFMGDFDASFVSGLWCIEPHVPKQEPDSPVLDPDSFVNEFLQVEGESSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNPRKRFPAEPSTTSSSSSSSSSENSGGRKKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVVGTPPEAAAGGGCSKDWNRYKGVRRRPWGKFAAEIRDPKKKGSRIWLGTYETPEDAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.1%;
ilarity 33.8%;
Conservative 3
                                                                                                                                                               Conservative
                                                                                                                                                                                26.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ridley, P.; Hudson, S.; Bancroft, Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
                                                                                                                                                               20;
                                                                                                                                                           Score 282.5; DB 2;
Pred. No. 2.4e-17;
0; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 286.5; DB
Pred. No. 1.3e-17
4; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202
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                                                                                                                                                               Indels
                                                                                                                                                                                                 Length
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  - VDARHYRGVRRRPWGKF
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                                                                                                                                                                                                        207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mewes, H.W.; Rudd,
                                                                                                                                                               33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51;
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  121
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C;Species: Lycopersicon esculentum (ton C;Date: 14-May-1999 #sequence_revision C;Accession: T07689
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R;Bevan, M.; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Hoheisel, J.; Mewes, H.W.;
submitted to the Protein Sequence Database, February 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F10M10.180 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: transcription factor
A;Note: binds the GCC box, present in the promoter region of genes encoding pathogenes:
C;Keywords: DNA binding; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ś
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  밁
                                                                                                                             5
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A;Experimental source: cultivar Columbia; BAC clone F10M10
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: Z15384
A; Accession: T04787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: The Pto kinase conferring resistance to tomato bacterial A; Reference number: Z16096; MUID:97357308; PMID:9214637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Zhou, J.; Tang, X.; Martin
EMBO J. 16, 3207-3218, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-268 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-161 < ZH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: T07689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription factor Pti5 - tomato
                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                           Map position: 4
Note: F10M10.180
                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 EI---VNASVSVD-KLSLCSNSYTTNNNSDSSLNEVSSG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 LIGSNISGPVRVNPRKRFPAEPSTTSSSSSSSSSSENSGG 197
                                                                                       55
                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lycopersicon esculentum (tomato)
                                 84 ---PPEAAAGGGCSKDWNR---YKGVRRRPWGKFAABIRDPKKKGSRIWLGTYETPEDAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 RYKGVRRRPWGKFAABIRDPKKKKGSRIWLGTYETPEDAALAYDAAAFNMRGAKARLNFPH 158
                                                                                                                                                                                   70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-161 <ZHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                               n 25.1%; Score 265.5; DB
Similarity 37.8%; Pred. No. 1e-15;
70; Conservative 25; Mismatches 4
SPVAKKAEGGGKIRKRKNKKNGYRGVRQRPWGKFAAEIRDP-KRATRVWLGTFETAEDAA
                                                                                  SDSTVISAGMPRLDSDTCQV-CRIEGCLGCNYFFAPNQRIEKNHQQEEEITGSSNRRRES 113
                                                                                                                                    SGSEIQKRGSP--SSESCQSNSMAESC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KYRGVRRPWGKYAAEIRDSARHGARVWLGTFETAEEAALAYDRAAFRMRGAKALLNFPS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKRKRSDVHEELQRTQSNSSSSSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVNPRKRFPAEPSTTSSSSSSSSSE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAEIRDPAKKGSRIWLGTFESDVDAARAYDCAAFKLRGRXAVLNFP-LDAGKYEAPANSG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAEIRDPKKKGSRIWLGTYETPEDAALAYDAAAFNMRGAKARLNFPHLIGSNISGPV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X.; Martin, G.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNIPROT:004681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.1%; Score 266; DB 2; 55.6%; Pred. No. 4.9e-16; tive 17; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL:U89256; NID:g2213782; PIDN:AAC49740.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-May-1999 #text_change
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                                                                                                                                                                                 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                 Indels
                                                                                                                                                                                                                         Length 268;
                                                                                                                                    ----QEDSVVGT-----
                                                                                                                                                                                 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-Jul-2004
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28 DSSSELTSTEENWEEIFADFLNWSGSEIQKRGSPSSESCQSNSMAESCQEDSVVGTPPEA 87

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RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Wh Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay, C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Binn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                   M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Taleuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vonature 402, 761-768, 199
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable AP2 domain transcription factor [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                              A; Map position: 2
                                                                                                                                                                                                   A; Cross-references:
                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-218 < STO>
                                                                                                                                                                                                                                                                              A;Accession: F84748
A;Status: prelimina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: F84748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT: P93822; GB:AE005172; NID:g1903358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA A; Residues: 1-133 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Lin, X.; Kaul,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: D86175
                                                                                                                                           Gene: At2g33710
                                                                                                                                                                   Genetics
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Best Local
  Matches
                             Best Local
                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 -NSGG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 MRGAKARLNEPHLIGSNISGPVRVNPRKREPAEPSTTSSSSSSSSSS 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 AAAGGGCSKDWNRYKGVRRRPWGKFAAEIRDPKKKGSRIWLGTYETPEDAALAYDAAAFN 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 SSGSGGGGAEQGKYRGVRRRPWGKYAAEIRDSRKHGERVWLGTFDTAEDAARAYDRAAYS 66
                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAYDRAAIGFRGPRAKLNFPFVDYTSSVSSPVAADD---IGAKASASASVSATDSVEAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MRGKAAILNFPHEYNMGTGS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; fat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                UNIPROT: P93007;
                             24.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.9%; Score 263; DB 2;
47.7%; Pred. No. 7.1e-16;
tive 17; Mismatches 25
24;
                             Score 263; DB 2;
Pred. No. 1.3e-15;
                                                                                                                                                                                             GB:AE002093; NID:g1707016; PIDN:AAC69127.1; GSPDB:GN
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSTAANSSSSSSQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P.; Southwick, A.M.; Sun,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               iel, N.A.; Kaul, S.; White, O.; Alonso, Conway, A.R.; Creasy, T.H.; Dewar, K.,
                                                    Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
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  30;
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Qy 88 AAGGGCSKDWNRYKGVRRRPWGKFAAEIRDPKKKGSRIWLGTYETPEDAALAYDAAAFNM 147	Qy 88 AAGGGCSKDWNRYKGYRRPPWGKPAAE  Db 64NSRQRNYRGYRRPPWGKWAAE  Qy 148 RGAKARLNPPHIIGSNISGPVRVNPRKI Db 117 RGHKAKLNPPEHIRVNPTQI RESULT 14 T02434 DNA binding protein BREBP-4 - common tobac C;Species: Nicotiana tabacum (common tobac C;Date: 05-Mar-1999 #sequence_revision 05- C;Accession: T02434 R;Ohme-Takagi, M.; Shinshi, H. Plant Cell 7, 173-182, 1995 A;Reference number: Z14671; MUID:95276459 A;Reference number: Z14671; MUID:95276459 A;Reference number: ACHYO A;Residues: 1-291 -COHYO A;References: UNIPROT:Q40478; EMBL:1 A;Residues: 1-291 -COHYO C;Species: Arabidopsis thaliana (mouse-ea) C;Specie	VERREPMEKHAAEIRDEKKKGSRIWLGTYETEEDAALAYDAAFUM   :    :    :    :     :
	148 117	LIGSNISGPVRVNPRKRFPAEPSTT      :    :  : HIRVNPTQLYPS-PATS
148 RGAKARLNFPHLIGSNISGÞVRVNÞRKRFÞAEÞSTT	RESULT 14 T02434 T02434 DNA binding protein ERE C;Species: Nicotiana tz C;Accession: T02434 R;Ohme-Takagi, M.; Shir Plant Cell 7, 173-182, A;Title: Ethylene-induc A;Recession: T02434 A;Recession: T02434 A;Status: preliminary;	common tobacco (common tobacco) _revision 05-Mar-1999 #text_change 09-Jul-2004 
NISGPVRVNPRKRFPAEPSTT 183HIRVNPTQLYPS-PATS 143HIRVNPTQLYPS-PATS 143  common tobacco (common tobacco) _revision 05-Mar-1999 #text_change 09-Jul-2004 _revision 05-Mar-1999 #text_tohange 09-Jul-2004	A;Status: preliminary, A;Molecule type: mRNA A;Residues: 1-291 <ohms A;Cross-references: UNI A;Experimental source: C;Superfamily: Arabidop</ohms 	ated from GB/EMBL/DDBJ 40478; EMBL:D38125; NID:g790361; PIDN:BAA07323.1; BY4; tissue-type leaf aliana hypothetical protein T19P19.170
148 RGAKARLNFPHLIGSNISGPVRVNPRKRFPAEPSTT 183	atch	Score 262.5; DB 2; Length 291; Pred. No. 2e-15; 28; Mismatches 63; Indels 97; Gaps
NISGPVRVNPRKRFPAEPSTT 183 :    : : : : : : : : : : : : : : : : :	14 11	MEHYCPQPILYSQSSSSSSELTSTEENWEEIFAD
NISGPVRVNPRKRFPAEPSTT 183 HRVNPTQLYPS-PATS 143  common tobacco (common tobacco) (common tobacco) (common tobacco) (revision 05-Mar-1999 #text_change 09-Jul-2004  .  NA binding proteins that interact with an ethylene UID:95276459; PMID:7756828  ated from GB/EMBL/DDBJ  40478; EMBL:D38125; NID:g790361; PIDN:BAA07323.1; BY4; tissue-type leaf BY4; tissue-type leaf BY4; tissue-type leaf BY4; Pred. No. 2e-15; BY5; Mismatches 63; Indels 97; Gaps 9;SDDSSELTSTEENWEEIFAD 46	47 71	
NISGPVRVNPRKRFPAEPSTT 183HIRVNPTQLYPS-PATS 143  COMMON tobacco (common tobacco (common tobacco) _revision 05-Mar-1999 #text_change 09-Jul-2004 _revision 05-Mar-1	74 131	PEAAAGGGCSKDWNRYKGVRRRPWGKFAAEIRDPKKKGSRIWLGTYETP :
NISGPVRVNPRKRFPAEPSTT 183HRVNPTQLYPS-PATS 143  common tobacco (common tobacco) (common tobacco) (common tobacco) (common tobacco)  revision 05-Mar-1999 #text_change 09-Jul-2004  _revision 05-Mar-1999 #text_change 09-J	134 179	HLIGSNISGPVR :: EVANFKQQDNBILQPANSGRKRMRETENEEIVIKK
NISGPVRVNPRKRFPAEPSTT 183 HIRVNPTQLYPS-PATS 143  common tobacco (common tobacco) _revision 05-Mar-1999 #text_change 09-Jul-2004 _revision 05-Mar-1999 #text_change 09-Jul-2004  .  NA binding proteins that interact with an ethylene UID:95276459; PMID:7756828  ated from GB/EMBL/DDBJ  ated from GB/EMBL/DDBJ  ated from GB/EMBL/DDBJ  8%; Score 562.5; DB 2; Length 291; A\$7; Pred. No. 2e-15; 28; Mismatches 63; Indels 97; Gaps 9;SDDSSELTSTEENWEEIFAD 46 EHYCPQPILYSQSSSSESINSIASELNNETFSFEPTLKYADTAQ 70  -WSGSEIQKRGSPSSESCQSNS	170 239	
COMMON tobacco (common tobacco) (common tobacco) (common tobacco) (common tobacco) (common tobacco) (common tobacco) (revision 05-Mar-1999 #text_change 09-Jul-2004 .  NA binding proteins that interact with an ethylene UID:95276459; PMID:7756828  ated from GB/EMBL/DDBJ  40478; EMBL:D38125; NID:g790361; PIDN:BAA07323.1; BY4; tissue-type leaf aliana hypothetical protein T19P19.170  aliana hypothetical prot	RESULT 15 B84718 CySpecies: Arabidopsis CySpecies: Arabidopsis CyAccession: B84718 CyAccession: B84718 R;Lin, X, KRUL, S.; Rc M.; Reiman, W.C. A; Reference number: A88 A; Rcession: B84718 A; Status: preliminary A; Molecule type: DNA A; Cross-references: UN1 C; Genetics:	- Arabidopsis thaliana ( cress) ( cress) ( T.P.; Benito, M.I.; Town, C.D.; Fujii hen, M.; Vannken, S.E.; Umayam, L.; Ta J.A.; Salzberg, S.L.; Fraser, C.M.; V mme 2 of the plant Arabidopsis thaliana ; PMID:10617197

Search completed: February 27, 2005, 22:06:51 Job time : 41 secs

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Result
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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Sequence 175489,
Sequence 34, Appl
Sequence 34, Appl
Sequence 416, App
Sequence 2074, App
Sequence 1832, App
Sequence 1832, App
Sequence 1832, App
Sequence 41687, App
Sequence 208822,
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## ALIGNMENTS

RESULT 1 US-10-225-068-128

Sequence 128, Appublication No.

Application US/10225068 b. US20030217383A1

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GENERAL INFORMATION:
APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: Reuber, T. Lynne
APPLICANT: Riechmann, Jose Luis
APPLICANT: Heard, Jacqueline E.
APPLICANT: Heard, Jacqueline E.
APPLICANT: Heard, Jacqueline E.
APPLICANT: Dubell, Arnold T.
APPLICANT: Dubell, Arnold T.
APPLICANT: Pineda, Omaira
APPLICANT: Pineda, Omaira
APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: Pineda, Omaira
CURRENT APPLICATION NUMBER: G0/10/225,068
CURRENT APPLICATION NUMBER: G0/310,847
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR APPLICATION NUMBER: 60/316,049
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR PILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 246
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 128
LENGTH: 226
TYPE: PRT
ORGANISM: Arabidopsis thaliana
PEATURE:
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; LOCATION: (89)...(157)
; OTHER INFORMATION: Conserved domain
US-10-225-068-128
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                                                                            ; OTHER INFORMATION: G22
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PRIOR FILING DATE: 2001-04-18
PRIOR PELICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/934,455
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 2001-08-22
PRIOR PELICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
                                                                                                                                                                        PRIOR APPLICATION NUMBER: 10/225,068
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 226
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Best Local :
Query Match 33.7%; Score 356.5; DB 15; Best Local Similarity 61.1%; Pred. No. 7.6e-27; Matches 69; Conservative 15; Mismatches 26;
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TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP
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                                                                                                               LENGTH: 226
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 10/225,067 FILING DATE: 2002-08-09
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 10/171,468 FILING DATE: 2002-06-14 APPLICATION NUMBER: 10/225,066 FILING DATE: 2002-08-09
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2001-11-19
APPLICATION NUMBER: 60/338,692
FILING DATE: 2001-12-11
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Similarity 61.1%; Pred. No. 7.6e-27;
69; Conservative 15; Mismatches 26
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Dubell III, Arnold T
Pineda, Omaira
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Ratcliffe, Oliver
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Jiang, Cai-Zhong
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                                                                                               (conserved domain in AA coordinates:
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                                                                                         ; OTHER INFORMATION: G22
US-10-412-699B-28
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                                                                                                                                                                                                                SOFTWARE: P.
SEQ ID NO 28
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Best Local Similarity 61.1%; Score 356.5; Matches 69; Conservative 15. Minimum 7.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ratcliffe, Oliver
APPLICANT: Kumimoto, Roderick
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MBI-0048CIP
CURRENT FILING DATE: 2003-04-10
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 09/394,519
PRIOR APPLICATION NUMBER: 09/394,519
PRIOR APPLICATION NUMBER: 09/489,376
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
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PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,392
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,029
PRIOR REPLICATION NUMBER: 09/533,029
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NUMBER OF SEQ ID NOS: 2011
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/713,994
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 09/819,142
PRIOR FILING DATE: 2001-03-27
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                                                                                                                         LENGTH: 226
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
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APPLICATION NUMBER: 09/532,591
FILING DATE: 2000-03-22
APPLICATION NUMBER: 09/533,648
FILING DATE: 2000-03-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 AAAFNMRGAKARLNFPHLIGSNISGPVRVNPRKRFPAEPSTTSSSSSSSSSEN 194
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                                                                                                                                                                                                                                         PatentIn
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Reuber, T. Lynne
Keddie, James S.
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Adam, Luc J.
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Jiang, Cai-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/10412699B
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                                                                                                                                                                                                                                                                             Application data removed -
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                                                DB 15; Length 226;
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US-10-424-599-175489
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 175489
LENGTH: 202
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
                                                                                                                                                                                                                                                                                                      Sequence 503, Application US/10374780A Publication No. US20040019927A1
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Best Local Similarity
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102
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                                                                                                                                                                                                                                                                                                                                                                                                                      162
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                                                                                                                                                                                     Riechmann, Jose Luis
Jiang, Cai-Zhong
Heard, Jacqueline E
Haake, Volker
                                                                                                                                                                                                                                                                                                                                                                                                                    SSPSSSCSDDSSESQGTKRRK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VWLGTYDTEEKAALAYDKAAFKMRGQKAKLNFPHLIDSDNSDELSEPVMMTTSKRSLLEI 161
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                                                                         Reuber, T. Lynne
Keddie, James
Broun, Pierre E
                   Pilgrim, Marsha L
Dubell III, Arnold T
Pineda, Omaira
                                                                                                                                Ratcliffe, (
                                                                                                                                                                     Creelman, Robert A
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 Guo-Liang
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Pred. No. 7.4e-27;
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Matches
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 503
LENGTH: 282
TYPE: PRT
ORGANISM: Mesembryanthemum crystallinum
FEATURE:
                                                                                                                                                                                                                                                                                                    Sequence 34, Application US/09533029
Publication No. US20030046723A1
                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                   APPLICANT: Heard, Jacqueline
APPLICANT: Broun, Pierre
APPLICANT: Riechmann, Jose-Luis
APPLICANT: Keddie, James
APPLICANT: Pineda, Omaira
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PRIOR
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PRIOR
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PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/934,455
                                                       APPLICANT:
                                                                                                                                                    APPLICANT:
                     ITLE OF I
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E OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES REFERENCE: MBI-010
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FILING DATE: 2001-11-19
APPLICATION NUMBER: 60/338,692
FILING DATE: 2001-12-11
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FILING DATE: 2002-08-09
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                                                                                                                                                                                                                                                                                                                                                                                                                    182
                                                                                                                                                                                                                                                                                                                                                                                                                                        144 AFNMRGAKARLNFPHLIGSNISGPVRVNPRKRFPAEPSTTSSSSSSSSSSSSSSSGRKK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 SEDMVLFGVLRDAVHTGWSPQSGSE-SGSGSPAPVTVKPEPV-----DSPVSSPAPVRV 121
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                                                   : Yu, Guo-Liang
: Ratcliffe, Oliver
: Pilgrim, Marsha
: Jiang, Cai-Zhong
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                                     Reuber, Lynne
                                                                                                                            Samaha, Raymond
Zhang, James
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEEIF-----ADFLNW---SGSEIQKRGSPSSESCQSNSMAESCQEDSVVGTP-PEAA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDFAVLESIRRHLLEDWDPRAGAPAITTGSGPVYHRNSSFSSLYPCLTDNWGELPLKEDD
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; APPLICANT: Pineda, Omaira
; TITLE OF INVENTION: Genes for Modifying Plant Traits IV
; FILE REFERENCE: MB1-0025
; CURRENT APPLICATION NUMBER: US/09/934,455
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227439
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: MB1-0022
; PRIOR APPLICATION NUMBER: MB1-0023
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: MB1-0023
; PRIOR FILING DATE: 2001-17
                                                                   ; TYPE: PRT; ORGANISM: Arabidopsis US-09-934-455-416
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                                                                                                                                      SEQ ID NO 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 34
LENGTH: 243
              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
 Matches 85;
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CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin Ver: 2.1
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APPLICANT:
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APPLICANT:
APPLICANT:
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NUMBER OF SEQ ID NOS: 516
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                                                                                                                      ENGTH: 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDYALLESITRHLLGGGGE---NELRLNESTPSSCFTE--SWGGLPLKENDSEDMLVYGL
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                                                                                                                                                                                                                                                                                                                                                                                Reuber, Lynne
Riechmann, Jose Luis
Yu, Guo-Liang
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Ratcliffe, Oliver
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Jiang, Cai-Zhong
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o. US20030121070A1
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Arnold
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31.9%; Score 338; DB 10; 39.4%; Pred. No. 5.7e-25; tive 30; Mismatches 69;
                                                                                     thaliana
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Pred. No. 9
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32;
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                                                                                    ; FEATURE:
; OTHER INFORMATION:
US-10-374-780A-2074
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PRIOR PRILOATION NUMBER: 60/310,847
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-22
PRIOR PPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-12-11
PRIOR PILING DATE: 2001-12-11
PRIOR PILING DATE: 2001-12-11
PRIOR PILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
Query Match
Best Local Similarity
Matches 85; Conser
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                                                                                                                                                                                                       SEQ ID NO 2074
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APPLICANT:
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CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YU, GUO-LIANG
TITLE OF INVENTION: POLYMUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP
                                                                                                                                                                                                                                            PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sherman, Bradley
                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 10/225,068
                                                                                                                                                                                                                                                                                                                                            PRIOR
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                                                                                                                                     LENGTH: 243
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 10/225,066
FILING DATE: 2002-08-09
APPLICATION NUMBER: 10/225,067
FILING DATE: 2002-08-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 -PSSESCQSNSMAESCQED-----SVVGTPPEAAAGGGCSKDWNRYKGVRRR
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Jiang, Cai-Zhong
Heard, Jacon
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Dubell III, Arnold T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratcliffe,
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Broun, Pierre E
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          31.9%;
ilarity 39.4%;
Conservative 3
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                                                                                                        Paralogous
          Score 338; DB 15;
Pred. No. 5.7e-25;
0; Mismatches 69;
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                                                                                                          G28
                                              Length 243;
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                                                                             SEQ ID NO 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/394,519
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 09/489,376
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: 09/506,720
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
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                                                                                                                         Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 2011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: MBI-0048CIP
CURRENT APPLICATION NUMBER: US/10/412,699B
CURRENT FILING DATE: 2003-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
LENGTH: 243
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                   APPLICATION NUMBER: 09/819,142 FILING DATE: 2001-03-27
                                                                                                                                                                                                           APPLICATION NUMBER: 09/713,994 FILING DATE: 2000-11-16
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/533,648
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/532,591
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/533,029
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                                                                                                  PatentIn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDYALLESITRHLLGGGGE---NELRLNESTPSSCFTE--SWGGLPLKENDSEDMLVYGL
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Kumimoto, Roderick
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Keddie, James S.
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Heard, Jacqueline E.
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iang, Cai-Zhong
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APPLICANT: Ratcliffe, Oliver
APPLICANT: Kunimoto, Roderick
APPLICANT: Kunimoto, Roderick
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: Polynuclectides and Polypeptides in Plants
FILE REFERENCE: MBI-0048CIP
CURRENT APPLICATION NUMBER: US/10/412,699B
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 09/394,519
PRIOR APPLICATION NUMBER: 09/394,519
PRIOR APPLICATION NUMBER: 09/489,376
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: 09/56,720
PRIOR APPLICATION NUMBER: 09/533,030
PRIOR APPLICATION NUMBER: 09/533,030
PRIOR FILING DATE: 2000-03-22
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US-10-412-699B-1832
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Best Local 9
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                                       OR APPLICATION NUMBER: 09/533,392
OR FILLING DATE: 2000-03-22
OR APPLICATION NUMBER: 09/533,029
OR FILLING DATE: 2000-03-22
OR APPLICATION NUMBER: 09/532,591
OR APPLICATION NUMBER: 09/532,691
OR FILING DATE: 2000-03-22
OR APPLICATION NUMBER: 09/533,648
OR APPLICATION NUMBER: 09/713,994
OR APPLICATION NUMBER: 09/713,994
FILING DATE:
APPLICATION |
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DuBell, Arnold N.
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Heard, Jacqueline E.
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Keddie, James S.
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Pred. No. 5.7e-25;
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US-10-425-114-41687
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LENGTH: 243
                                                                                                                                                                                                                                                                                                                   Best
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Best Local
                                                                                                                                                                                                                                                                                                 Matches
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                   Similarity
PVRVNPRKRFPAEPSTTSSSSSSSSSENSGGRKKRR 202
                                                          PWGKFAAEIRDPAKNGARVWLGTFETAEDAALAYDIAAFRMRGSRALLNFPLRVNSGEPD 188
                                                                                               PWGKFAABIRDPKKKGSRIWLGTYETPEDAALAYDAAAFNMRGAKARLNFPHLIGSNISG 166
                                                                                                                                                                                                                  SDYALLESITRHLLGGGGE---NELRLNESTPSSCFTE--SWGGLPLKENDSEDMLVYGL 68
                                                                                                                                                                                                                                                          SDRFLLSLIEEHLLSDNSDDSSSELTSTEENWEEIFADFLNWSGSEIQKRGS------
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                                                                                                                                                                                                                                                                                             Score 338; DB 15; Length 248; Pred. No. 5.8e-25; O; Mismatches 69; Indels 3
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US-10-424-599-208822; Sequence 208822, Application US/10424599; Publication No. US20040031072A1
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                                                                                     ; OTHER INFORMATION: Clone ID: 700237304_FLI.pep US-10-425-114-43402
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                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 43402
LENGTH: 311
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LENGTH: 156
TYPE: PRT
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Publication No. US20040034888A1
                   Query Match
Best Local
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APPLICANT:
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  Matches
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Dav
                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B
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                                                                                                                              FEATURE:
                                                                                                                                           TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 FNMRGAKARLNFPHLIGSNI 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 PVRITSKR---SSSSSSSSSSSSSSEN--GKLKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 FNMRGQKAKLNFPHLIGSGV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 PEAAAGGGCSKDWNRYKGVRRRPWGKFAAEIRDPKKKGSRIWLGTYETPEDAALAYDAAA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 SSELTSTEENWEEIFADFLNWSGSEI----QKRGSPSSESCQSNSM-AESCQEDSVVGTP
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  90; Conservative
                                                                                                                                                                                                                                                                                                                                             Zhou, Yihua
Kovalic, David K.
Screen, Steven E
: Tabaska, Jack E
: Cao, Yongwei
: Cao, Yongwei
                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.3%;
31.2%; Score 330.5; DB 15; 36.9%; Pred. No. 4.4e-24; tive 29; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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Pred. No. 1.4e-24;
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  Indels
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                                           311;
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9 SDRFLLSLIEEHLLSDNSDDSSSELTSTEENWEEIFADFLNWSGS--

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APPLICANT: Pilgrim, Marsha
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heuber, Lynne
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-010
CUURRENT APPLICATION NUMBER: US/09/533,029
CUURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 268
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Best Local Similarity
Watches 91; Conserve
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US-09-533-029-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application US/09533029 Publication No. US20030046723A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Keddie, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Heard, Jacqueline
APPLICANT: Broun, Pierre
APPLICANT: Riechmann, Jose-Luis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pineda, APPLICANT: Adam, L
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APPLICANT: Ratcliffe, Oliver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
  178
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                                                                                                                                                          61 YPCFTESWGDLPLKENDSEDMLVYGILNDAFHGGWEPSSSSSSDEDRSSFPSVKIETPESF 120
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                          YETPEDAALAYDAAAFNMRGAKARLNFPHLIGSNISGPVRVNPRKRFPAEPSTTSSSSSS 189
                                                                            AAVDSVPVKKEKTSPVSAAVTAAKGK---HYRGVRQRPWGKFAAEIRDPAKNGARVWLGT 177
                                                                                                     SMAESCQEDSVVGTPPEAAAGGGCSKDWNRYKGVRRRPWGKFAAEIRDPKKKGSRIWLGT 129
                                                                                                                                                                                                                                                                        MSEEIISVSDRFLLSLIEEHLLSDN----SDDSSSELTST--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----PEAAAGGGCSKDWNRYKGVRRRPWGKFAAEIRDPKKKGSRIWLGTYETPEDAAL 138
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FETAEDAALAYDRAAFRMRGSRALLNFPLRVNSGEPDPVRIKSKR---
                                                                                                                                                                                              ----EENW-----EEIFADFL------NW----SGSEIQKRGSPS--SESCQSN 69
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                                                                                                                                                                                                                                                                                                               30.6%; Score 324; DB 10; ilarity 36.0%; Pred. No. 1.6e-23; Conservative 27; Mismatches 69;
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Search completed: February 27, Job time : 131 secs
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SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 268
TYPE: PRT
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APPLICANT: Creelman,
APPLICANT: Dubell, Ar
APPLICANT: Heard, Jac
APPLICANT: Jiang, Cai
APPLICANT: Keddie, Jan
APPLICANT: Pilgrim, M
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Publication No. US20030121070A1
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APPLICANT:
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CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Reuber, Lynne
APPLICANT: Riechmann, Jose Luis
APPLICANT: Yu, Guo-Liang
APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits
FILE REFERENCE: MBI-0025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: MBI-0023 PRIOR FILING DATE: 2001-04-17
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                                                                                                                                                                                                                                                                                                                                                                                                    1 MSEEIISVSDRFLLSLIEEHLLSDN----SDDSSSELTST-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 30.6%; Score 324; DB 10; Similarity 36.0%; Pred. No. 1.6e-23;
                                                                      SSNEN-GAPKKRR
                                                                                                      SSSENSGGRKKRR 202
                                                                                                                                            FÉTAEDAALAYDRAAFRMRGSRALLNFPLRVNSGEPDPVRIKSKR--
                                                                                                                                                                                                                  AAVDSVPVKKEKTSPVSAAVTAAKGK---HYRGVRQRPWGKFAAE
                                                                                                                                                                                                                                                      SMAESCQEDSVVGTPPEAAAGGGCSKDWNRYKGVRRRPWGKFAAEIRDPKKKGSRIWLGT 129
                                                                                                                                                                                                                                                                                        YPCFTESWGDLPLKENDSEDMLVYGILNDAFHGGWEPSSSSSDEDRSSFPSVKIETPESF
                                                                                                                                                                                                                                                                                                                              ----EENW-----EEIFADFL-----NW----SGSEIQKRGSPS--SESCQSN 69
                                                                                                                                                                                                                                                                                                                                                                MSMTADSQSDYAFLESIRRHLLGESEPILSESTASSVTQSCVTGQSIKPVYGRNPSFSKL
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Dubell, Arnold
Heard, Jacqueline
Jiang, Cai-Zhong
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Ratcliffe, Oliver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61:
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0 seq length: 2000000000
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Maximum Match 100%
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen
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US-08-949-603-11
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US-08-949-580-11
US-08-949-580-11
US-08-950-172A-11
US-08-950-172A-11
US-08-950-1802D-13
US-09-601-802D-13
US-09-601-802D-13
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US-09-601-802D-13
US-09-601-802D-13
US-09-61-272-17
US-09-202-161B-25
US-09-202-161B-25
US-09-202-161B-26
US-09-533-029-22
US-09-640-211A-810
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US-09-640-211A-761
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      Sequence 34, Appl
Sequence 1, Appl
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Sequence 9, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 26, Appl
Sequence 27, Appl
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Sequence 27, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 1, Appl
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US-08-912-272-24 US-08-912-272-21 US-08-912-272-25 US-08-912-272-25 US-09-026-039-21 US-08-912-272-2 US-09-026-039-25 US-09-026-039-22 US-09-026-039-22 US-09-026-039-22 US-09-026-039-22 US-09-640-211A-838 US-09-300-672-10 US-09-300-672-2 US-09-300-672-2	w	ω	4	4	4	4	w	4	ω	ω	w	ω	w	w	w	w	w
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	App1	Appli	App1	i ldd	Appli	ippli	, Appl	838, App	Appl	Appl	ilgqr	Appl	Appl	Appl	Appl	App1	Appl

ALIGNMENTS

## ; OTHER INFORMATION: G1006 US-09-533-029-34 US-09-533-029-34 APPLICANT: Heard, Jacqueline APPLICANT: Broun, Pierre APPLICANT: Riechmann, Jose-Luis APPLICANT: Keddie, James APPLICANT: Pineda, Omaira APPLICANT: Samaha, Raymond APPLICANT: Samaha, Raymond APPLICANT: Samaha, James CURRENT APPLICATION NUMBER: US/09/533,029 CURRENT FILING DATE: 2000-03-22 EARLIER APPLICATION NUMBER: 60/125,814 EARLIER FILING DATE: 1999-03-23 NUMBER OF SEQ ID NOS: 121 SOFTWARE: PATENTIN Ver. 2.1 SEQ ID NO 34 LENGTH: 243 Query Match GENERAL INFORMATION: Sequence 34, Appli Patent No. 6664446 APPLICANT: Yu, Guo-Liang APPLICANT: Ratcliffe, Oliver APPLICANT: Pilgrim, Marsha APPLICANT: Jiang, Cai-Zhong APPLICANT: Reuber, Lynne TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES FILE REFERENCE: MBI-010 TYPE: PRT ORGANISM: Arabidopsis thaliana FEATURE: Local 107 PWGKFAAEIRDPKKKGSRIWLGTYETPEDAALAYDAAAFUMRGAKARLNFPHLIGSNISG 64 LKDAFHFDTSSSDLSCLFDFPAVKVEPTENFTAMEEKPKKAIPVTETAVKAKHYRGVRQR 61 -PSSESCQSNSMAESCQED------SVVGTPPEAAAGGGCSKDWNRYKGVRRR 9 9 SDRFLLSLIEEHLLSDNSDDSSSELTSTEENWEEIFADFLNWSGSEIQKRGS------85; h 31.9%; Score 338; DB 4; Length 243; Similarity 39.4%; Pred. No. 3.3e-30; 85; Conservative 30; Mismatches 69; Indels SDYALLESITRHLLGGGGE---NELRLNESTPSSCFTE--SWGGLPLKENDSEDMLVYGL Application US/09533029

124

PWGKFAAEIRDPAKNGARVWLGTFETAEDAALAYDIAAFRMRGSRALLNFPLRVNSGEPD

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106 63

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PVRITSKR---SSSSSSSSSSSSTSSSEN--GKLKRR 214 PVRVNPRKRFPAEPSTTSSSSSSSSSSENSGGRKKRR 202

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RESULT 3
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; APPLICANT: Pilgrim, Marsha
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOCTWARE: Daterin Ver 2 1
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                   Sequence 1, Application US/09202161B
Patent No. 6653533
GENERAL INFORMATION:
APPLICANT: Purdue Research Foundation
TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
FILE REFERENCE: 7024-371
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CURRENT APPLICATION NUMBER: US/09/202,161B
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APPLICANT: Adam, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Keddie, James
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Arabidopsis thaliana FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                  190
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                                                                                                                                                                                                                                                    227
                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AAVDSVPVKKEKTSPVSÅAVTAAKGK---HYRGVRQRPWGKFAAEIRDPAKNGARVWLGT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YPCFTESWGDLPLKENDSEDMLVYGILNDAFHGGWEPSSSSSDEDRSSFPSVKIETPESF 120
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                                                                                                                                                                                                                                                    SSNEN-GAPKKRR 238
                                                                                                                                                                                                                                                                                                  SSSENSGGRKKRR 202
                                                                                                                                                                                                                                                                                                                                               FETAEDAALAYDRAAFRMRGSRALLNFPLRVNSGEPDPVRIKSKR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMAESCQEDSVVGTPPEAAAGGGCSKDWNRYKGVRRRPWGKFAAEIRDPKKKGSRIWLGT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----EENW------EEIFADFL------NW----SGSEIQKRGSPS--SESCQSN 69
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               NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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Matches
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PRIOR FILING DATE: 1997-06-12
PRIOR APPLICATION NUMBER: 60/046,494
PRIOR FILING DATE: 1997-05-14
PRIOR APPLICATION NUMBER: 60/019,633
PRIOR FILING DATE: 1996-06-12
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                FILING DATE: 15-AUG-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 20-JUN-1997
PRIOR APPLICATION NUMBER: US 08/
APPLICATION NUMBER: US 08/
FILING DATE: 20-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII
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                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/912,272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jofuku, K. Diane APPLICANT: Okamuro, Jack K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 NFTAGEVKSEPREEIESSPEFS-----PSPAGT---TAAPAAETPKRRHYRGVRQRPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 NWSGSEIQKRGSPSSESCQSNSMAESCQEDSVVGTPPEAAAGGGCSKDWNRYKGVRRRPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
67; Conserva
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6093874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKFAAEIRDPAKNGARVWLGTYETAEEAAIAYDKAAYRMRGSKAHLNFPHRIGLNEPEPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   California
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69 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1999-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jack K.
Methods for Improving Seeds
                                                                                                                                                                                                                              US 08/700,152
                                                                                                                                                                                                                                                                                           US 08/879,827
                                                                                                                          023070-067220US
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RESULT 5
US-09-026-039-18
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
TELEFAX: (415) 576-03
                                                                                                                      APPLICATION NUMBER: US 08/700,152 FILING DATE: 20-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          APPLICATION NUMBER: US 08/879,827 FILING DATE: 20-JUN-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 15-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 103
                TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                               FILING DATE: 15-AUG-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Region LOCATION: 35..51 OTHER INFORMATION: OTHER INFORMATION:
                                                                    NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-067230US
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two Emparcad
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 IGSN 163
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76.6%;
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EREBP-2"
                                                                                                                                                                                                                                                                  US 08/912,272
                                                                                                                                                                                                                                                                                                                                        US/09/026,039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 274; DB 3; Length 69; Pred. No. 1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for Improving Seeds
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US-09-300-672-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Finkelstein, Ruth R.
APPLICANT: Lynch, Tim
APPLICANT: Goodman, Howard M.
APPLICANT: Goodman, Howard M.
APPLICANT: Geoman, Howard M.
APPLICANT: Wang, Ming-Li
ITILE OF INVENTION: A TRANSCRIPTION FACTOR REGULATING SEED DEVELOPMENT,
TITLE OF INVENTION: QUALITY AND COLD-TOLERANCE
FILE REFERENCE: 480.89(HY)
CURRENT APPLICATION NUMBER: US/09/300,672
CURRENT APPLICATION NUMBER: US/09/300,672
NUMBER OF SEQ ID NOS: 16
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 9: A
                                                                                                                                           Sequence 2, Application US/09202161B Patent No. 6653533 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
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CURRENT APPLICATION NUMBER: US/09/202,161B
CURRENT FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: PCT/US97/10382
PRIOR FILING DATE: 1997-06-12
PRIOR APPLICATION NUMBER: 60/046,494
                                                                                        APPLICANT: Purdue Research Foundation
TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
FILE REFERENCE: 7024-371
                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 60
TYPE: PRT
ORGANISM: AP2 domain protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
TOPOLOGY: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Peptide
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                                                                                                                                                                                                                                                                                               100 YKGVRRPPWGKFAAEIRDPKKKGSRIWLGTYETPEDAALAYDAAAFNMRGAKARLNFPH 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 IGSN 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 YKGVRRRPWGKFAAEIRDPKKKGSRIWLGTYETPEDAALAYDAAAFNMRGAKARLNFPHL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49;
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                                                                                                                                                                                                                                                                                1 YRGVRRRÞWGKFAAEIRDÞAKNGARVWLGTYETDEEAAIAYDKAAYRMRGSKAHLNFÞH 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 YRGVRORPWGKFAAEIRDPAKNGARVWLGTYETAEEAALAYDKAAYRMRGSKALLNFPHR
                                                                                                                                                                                                                                                                                                                                                                         Similarity
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78.0%;
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76.6%;
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alpha-helix"
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EREBP-2"
                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                   Score 266; DB 3;
Pred. No. 6.7e-23;
7; Mismatches 6
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Pred. No. 1e-23;
7; Mismatches
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LENGTH: 161
TYPE: PRT
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                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/706,270
FILING DATE: September 4, 1996
ATTORNEY, AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-384
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEPAX: (517) 347-4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1997-05-14
PRIOR APPLICATION NUMBER: 60/019,633
PRIOR FILING DATE: 1996-06-12
NUMBER OF SEQ ID NOS: 30
                                                                                                                                           TELEX: NO. 5891859e
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Michae
APPLICANT: Eric J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII
MOLECULE TYPE: Pol
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: MS.DOS 5
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                        POPOLOGY:
                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 EI---VNASVSVD-KLSLCSNSYTTNNNSDSSLNEVSSG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 LIGSNISGPVRVNPRKRFPAEPSTTSSSSSSSSSSENSGG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 KYRĞVRRRPWGKYAAEIRDSARHGARVWLGTFETAEEAALAYDRAAFRMRGAKALLNFPS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 RYKGVRRRÞWGKFAAEIRDÞKKKGSRIWLGTYETÞEDAALAYDAAAFNMRGAKARLNFPH 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55; Conservative
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Similarity 55.6%; Pred. No. 3e-22;
                                                                                                            Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eric J. Stockinger
VERVION: DNA AND ENCODED PROTEIN
VERVION: WHICH REGULATES COLD AND
VERVION: DEHYDRATION REGULATED GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Michael F. Thomashow and
                                                                      Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM Compatible
SYSTEM: MS-DOS 5.00
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                                                     Polypeptide
                                                                                       Single
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IDENTIFICATION METHOD: sequer
OTHER INFORMATION: Figure 2D
PUBLICATION INFORMATION:
US-08-949-603-11
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Best Local Similarity 78.0
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Patent No.
                                                              TELEX: NO. 5892009e INFORMATION FOR SEQ ID NO:
                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4103
TELEFAX: (517) 347-4103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Michael F. Thomashow and APPLICANT: Exic J. Stockinger TITLE OF INVENTION: DAA AND ENCODED PROTEIN TITLE OF INVENTION: WHICH REGULATES COLD AND TITLE OF INVENTION: DEHYDRATION REGULATED GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
ORGANISM: Tobacco
                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                      CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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HAPLOTYPE: N/A
TISSUE TYPE: N/A
CELL TYPE: N/A
CELL LINE: N/A
LENGTH: 61
TYPE: Amino Acid
STRANDEDNESS: Sir
                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: Septem
                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Michigan
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                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: MS-DOS 5.00
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5892009
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                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                 IBM Compatible
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                                                                                                                                                                                                                                                                   September 4, 1996
                                                                                                                                                                                                                                                                                                                                                                 storage
                                                                                                                                                                                                                                                                                                                                                                              Diskette,
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N/A
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78.0%;
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Pred. No. 2e-22;
7; Mismatches
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HYPOTHETICAL: N

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TOPOLOGY:

Linear

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Best Local Similarity
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/706,270
FILING DATE: September 4, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4103
TELEFAX: (517) 347-4103
TELEFAX: No. 5929305e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS 5.00
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Michael F. Thomashow and APPLICANT: Eric J. Stockinger TITLE OF INVENTION: DNA AND ENCODED TITLE OF INVENTION: WHICH REGULATES TITLE OF INVENTION: DEHYDRATION REGULATES NUMBER OF SEQUENCES: 11
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CELL LINE: N/A
ORGANELLE: N/A
IMMEDIATE SOURCE:
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 YKGVRRPWGKFAAEIRDPKKKKGSRIWLGTYETPEDAALAYDAAAFNMRGAKARLNFPH 158
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    Application US/08949580
5929305

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78.0%;
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Pred. No. 2e-22;
7; Mismatches
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Michael F. Thomashow and
APPLICANT: Eric J. Stockinger
                                                                                                                                                                        ZIP: 4864

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5
MEDIUM TYPE: storage
COMPUTER: IBM Companion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                     FILING FOR THE PRIOR PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/949,580
APPLICATION NUMBER: 08/706,270
FILING DATE: October 14, 1997
FILING DATE: 08/706,270
                                                                                                                                 OPERATING SYSTEM: MS-DOS:
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
THE /OR
                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION METHOD: sequent OTHER INFORMATION: Figure 2D PUBLICATION INFORMATION:
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ORIGINAL SOURCE:
ORGANISM: Tobacco
APPLICATION NUMBER: 08/70
FILING DATE: September 4,
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL STAGE DEVELOPMENTAL STAGE HAPLOTYPE: N/A
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MOLECULE TYPE: Po
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                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANELLE: N/A IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL TYPE:
CELL LINE:
ORGANELLE:
                                                                                                          APPLICATION NUMBER: US/08/950,172A FILING DATE: 10/14/1997
                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: Sir
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                 CITY:
                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 YKGVRRRPWGKFAABIRDPKKKGSRIWLGTYETPEDAALAYDAAAFNMRGAKARLNFPH 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 YRGVRQRPWGKFAAEIRDPAKNGARVWLGTYETAEEAALAYDKAAYRMRGSKALLNFPH
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46; Conservative
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                                                                                                                                                                                                                                                                                                 Okemos
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                                                                                                                                                                                       IBM Compatible
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                                                                                                                                                                       MS-DOS 5.00
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                                                                                                                                                                                                                                                                                                                Parkway
                                                                                                                                                                                                                      5.25 inch,
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Pred. No. 2e-22;
7; Mismatches
                                                                                                                                                                                                                      360
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60

MSU

4.1-383

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APPLICANT: Zarka, Daniel
APPLICANT: Jiang, Cai-Zhong
TITLE OF INVENTION: Plant Having Altered Environmental Stress Tolerance
FILE REFERENCE: 19117.713 Seq List
CURRENT APPLICATION NUMBER: US/09/198,119C
CURRENT FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: US 08/706,270
PRIOR APPLICATION NUMBER: US 09/018,233
PRIOR APPLICATION NUMBER: US 09/018,233
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/018,235
PRIOR PILING DATE: 1998-02-03
PRIOR PILING DATE: 1998-02-03
PRIOR PILING DATE: 1998-02-03
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REFERENCE/DOCKET NUMBER: MSU 4
REFERENCE/DOCKET NUMBER: MSU 4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4103
TELEPHONE: (517) 347-4103
TELEPHONE: 4965705e 11:
                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                             APPLICANT:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
IDENTIFICATION METHOD: sequer
OTHER INFORMATION: Figure 2D
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE TYPE: N/A
CELL TYPE: N/A
CELL LINE: N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANELLE: N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENTAL STAGE: HAPLOTYPE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Tobacco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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R APPLICATION NUMBER:
R FILING DATE: 1998-02
R APPLICATION NUMBER:
R FILING DATE: 1998-02
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                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
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                                                                                                                                                                                                                                                                                                                                                                                                                      1, Application US/09198119C 6417428
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Jaglo-Ottosen, Kirsten
                                                                                                                                                                                                                                                                                                                                                                                  Thomashow, Michael
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N/A
                                   1998-02-03
 1998-02-03
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78.0%;
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                    09/018,227
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Pred. No. 2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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TRESULT 14
US-09-601-802D-134
; Sequence 134, Application US/09601802D
; Patent No. 6706866
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                                                                                                                                                                                                                                                             US-09-601-802D-11
                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/198,119
PRIOR FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 259
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 11
LENGTH: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 11
LENGTH: 61
TYPE: PRT
ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09601802D
                                                                                                                                                                                     Matches 46;
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Best Local Similarity 78.0%;
                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Haake, Volker
TITLE OF INVENTION: STRESS TOLERANCE
TITLE OF INVENTION: STRESS TOLERANCE
FILE REFERENCE: 514442000201/MB10029
CURRENT APPLICATION NUMBER: US/09/601,802D
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/018,233
PRIOR APPLICATION NUMBER: 09/017,816
PRIOR APPLICATION NUMBER: 09/017,816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Thomashow, Michael APPLICANT: Stockinger, Eric APPLICANT: Jaglo-Ottosen, Ki APPLICANT: Gilmour, Sarah APPLICANT: Zarka, Daniel Zarka, Daniel
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PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: 09/018,235
PRIOR FILING DATE: 1998-02-03
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                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/018,234
PRIOR FILING DATE: 1998-02-03
                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/017,575
FILING DATE: 1998-02-03
APPLICATION NUMBER: 09/018,227
FILING DATE: 1998-02-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 YKGVRRRPWGKFAAEIRDPKKKGSRIWLGTYETPEDAALAYDAAAFNMRGAKARLNFPH
                                                                                                                                     100 YKGVRRRPWGKFAAEIRDPKKKGSRIWLGTYETPEDAALAYDAAAFNMRGAKARLNFPH 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stockinger, Eric
Jaglo-Ottosen, Kirsten
                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                     24.8%;
78.0%;
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Pred. No. 2e-22;
7; Mismatches
                                                                                                                                                                                                       Score 262; DB 4
Pred. No. 2e-22;
                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                        DB 4;
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                                                                                                                                                                                                                        Length 61;
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                                                                                                                                                                                       Indels
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GENERAL INFORMATION:

APPLICANT:

Stockinger, Eric Jaglo-Ottosen, Kirsten Gilmour, Sarah

Thomashow, Michael

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RESULT 15
US-08-912-272-17
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; ORGANISM: Nicotiana tabacum
US-09-601-802D-134
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Patent No. 6093874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 134
LENGTH: 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,272
FILING DATE: 15-AUG-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/879,827
FILING DATE: 20-JUN-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/018,235
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: 09/017,575
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: 09/018,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 514442000201/MBI0029
CURRENT APPLICATION NUMBER: U$/09/601,802D
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/018,233
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: 09/017,816
PRIOR FILING DATE: 1998-02-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zhang, James
APPLICANT: Haake, Volker
TITLE OF INVENTION: PLANT HAVING ALTERED ENVIRONMENTAL
TITLE OF INVENTION: STRESS TOLERANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESSE: Townsend and Townsend and Crew LLP
ADDRESSEE: Two Embarcadero Center, Eighth Floor
STREET:
                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/198,119
FILING DATE: 1998-11-23
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                                                                                                                                                                                                                                                                                                                                   California
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Jiang, Cai-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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78.0%;
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LOCATION: Region
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COTHER INFORMATION:
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US-08-912-272-17
Search completed: February 27, 2005, 22:07:39 Job time : 44 secs
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ATTORNEY/AGENT INFORMATION:
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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                                                            TYPE: amino a STRANDEDNESS: TOPOLOGY: lir
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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Copyright (c) 1993 - 2005 Compugen Ltd.
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AYDAAAFNMR         AYDAAAFNMR	SVVGTPPEAAA          SVVGTPPEAAA	EHLLSDNSD	; Score 20; ; Pred. No 0; Mismato	RT "ORCA3, a jasmonate-responsive transcril RT primary and secondary metabolism."; RL Science 289:295-297(2000).; RT SCIENCE 289:295-297(2000).; REMBL; AV251250; CAB96900.1; DR EMBL; AV251249; CAB96899.1; DR GOSIONARY CAB96899.1; DR TRANSFAC; T04751; DR GO; GO:000337; 2GCC. DR GO; GO:0003700; Frtranscription factor and control of transcription factor and control of transcript	894776; DO	eriwinkle) (Madagascar treptophyta; Embryophyt a; eudicotyledons; core naceae; Rauvolfioideae;	Created) Last seque Last annotes ein.	PRT;	ALIGN	Q6RZW7 Q6V3V8 Q8H075 Q9FR33 Q40479 Q04680 Q9LW50	Q9M9B2 Q6H6I3 Q949D2 Q7XAD6 Q7XAD6 Q9SZ06 Q7XU94 Q7XU93	
RGAKARLNFI         RGAKARLNFI	366CS	DSSSELTS 	3; DB . 4.8e ches	ption activ iptio	H	(Madag ta; Embr tyledons	ence u tation	203 AA.	ALIGNMENTS			
FPHLIGSNI          FPHLIGSNI	KOWNRYKGVRRRI            KOWNRYKGVRRRI	TEENWEEI	2; Lengt: -183; 0; Inde	l regul ty; IEA , DNA-d , CRC6	в/в	ascar pe yophyta; ; core e ideae; V	odate) update)					
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HSSP; O80337; 2GCC.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0006355; P:transcription of to
InterPro; IPR000977; DNA ligase.
InterPro; IPR001471; TP ERF
PRINTS; PR00367; ETHRSPELEMNT.
                                                                                                                                                             SEQUENCE FROM N.A. Rounsley S.D., Lin Sykes S.M., Mason T Venter J.C.;
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01-OCT-2002
01-MAR-2004
   SEQUENCE FROM N. Town C.D., Kaul Submitted (FEB-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification and characterization of a soybean ethylene-responsive element binding protein gene whose mRNA expression changes during soybean cyst nematode infection."; MOI. Plant Microbe Interact. 15:577-586(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     022167;
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Q8LLR3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative ethylene response element binding protein
response element binding protein; EREBP).
                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core exeurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SMART; SM00380; AP2; 1.
PROSITE; PS00697; DNA_LIGASE
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MEDLINE=22054140; PubMed=12059106;
Mazarei M., Puthoff D.P., Hart J.K.,
"Identification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
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   FROM N.A.
, Kaul S.;
i (FEB-2002)
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yta; eudicotyledons; core eudicots; rosid
ceae; Papilionoideae; Phaseoleae; Glycine
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transcription, DNA-dependent;
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R., Adams
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eudicots; rosids;
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Best Local S
Matches 19
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A Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
A Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kaw
A Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K
A Ecker J., Theologis A., Davis R.W.;
L Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AC002388; AAC31840.1; -.
R EMBL; AF325089; AAKX17157.1; -.
R EMBL; AF370540; AAKX17157.1; -.
R EMBL; AF370540; AAKX48967.1; -.
R HSSP; 080337; 2GCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8L9K1;
01-OCT-2002
01-OCT-2002
SEQUENCE FR
Brover V.,
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SOUTHWICK A., Karlin-Neumann G., Nguyen M., Lan
Southwick A., Karlin-Neumann G., Nguyen M., Lan
Falm C.J., Theologis A., Ecker J., Davis R.W.;
Palm C.J., Theologis A., Ecker J., Davis R.W.;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative ethylene response element binding protein
Putative thaliana (Mouse-ear cress).
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PRODOM; PD001423; TF ERF; 1.
SMART; SM00380; AP2; 1.
PROSITE; PS00697; DNA LIGASE A1;
SEQUENCE 226 AA; 25353 MW; 48
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                                                                                                  Haas B.J., Volfovsky N., To
Feldmann K.A., Flavell R.B.
"Full-length messenger RNA
annotation.";
                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosiceurosids II; Brassicales; Brassicaceae; Arabidopsis.
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GO; GO:0003700; F:transcription
GO; GO:0006355; P:regulation of
InterPro; IPR000977; DNA ligase.
InterPro; IPR001471; TF ERF
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                                                                           Genome
                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=22088475;
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                       FROM N.
  Troukhan
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                                                                           3:RESEARCH0029-RESEARCH0029(2002)
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5; PubMed=12093376;
ovsky N., Town C.D., Troukhan M.
ovsky N., White O., Salzberg
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  Alexandrov
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4B2EF81CDD856987
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Matches 18
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Best Local S
Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN-6.don; TISSUB-Cell suspension;

STRAIN-6.don; TISSUB-Cell suspension;

MEDIJINS-93380162; PubMed-10449411; DOI=10.1093/emboj/18.16.4455;

MEDIJINS-93380162; PubMed-10449411; DOI=10.1093/emboj/18.16.4455;

Menke F.L.H., Champion A., Kijne J.W., Memelink J.;

"A novel jasmonate- and elicitor-responsive element in the periwinkle secondary metabolite biosynthetic gene Str interacts with a jasmonate-
secondary metabolite biosynthetic gene Str interacts with a jasmonate-
and elicitor-inducible AP2-domain transcription factor, ORCA2.";
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InterPro; IPR001471; TF ERF:
PRINTS; PR00367; ETHRSPELLEMNT.
ProDom; PD001423; TF ERF; 1.
SMART; SM00380; AP2; 1.
PROSITE; P800687; DNA LIGASE A1; UNKNOWN 1.
SEQUENCE 226 AA; 25367 MW; C3F80438CFF19D80 CRC64;
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003770; F:transcription
GO; GO:0006355; P:regulation of
                                                                                                                                                                                                                                                                                                                                                                               DNA-binding.
210 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBO J. 18:4455-4463(1999).
EMBL; AJ238740; CAB93940.1; -.
HSSP; O80337; 2GCC.
TRANSFAC; T04749; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; aster
lamiids; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9LEM6;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00380; AP2; 1.
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                                                                                                                                                       GVRRRPWGKFAAEIRDPK 146
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ilarity 100.0%;
Conservative (
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   PRELIMINARY;
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                                                                                                                                                                                                                                                                         Score 18; DB; Pred. No. 1.8
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Pred. No.
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  017DF088F713CE38 CRC64;
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2.1e-09;
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   SO CERT TO DESCRIPTION OF THE PROPERTY OF THE 
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O1-OCT-2003 (TrEMBLrel. 25, Last sequence upont of the control of the cont
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Gramene; Q7XDZ; -...
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription f:
GO; GO:0006355; P:regulation of t:
InterPro; IPR001471; TP ERF.
ProDom; PD001423; TF ERF; 1.
                                                                                                                                        PubMed=12447439; DOI=10.1038/nature01183;
Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J., Feng Q., Zhang Y., Jia P., Zhao Q., Ying K., Yu S., Tang Y., Li Y., Hu X., Jia P., Zhang Y., Lu Y., Zhang L.S., Yu S., Tang Y., Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D., Li X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J., Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H., Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Jia J., Zhang Y., Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W., Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W., Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y., Lu Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
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Q6MWK9;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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                                                                                                                     Lan L.,
Han B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00380; AP2; 1.
Polyprotein.
SEQUENCE 124 AA; 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buell C.R., Wing R.A.,
Submitted (MAY-2003) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=39947;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=B1234D02.6
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   SEQUENCE FROM N.A.
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                                                                                           Sequence and analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 GVRRRPWGKFAAEIRDP 118
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17; Conserv
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                                                            420:316-320(2002)
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100.0%; Pr
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cture, activity, and ev
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                                                                                           rice
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Last
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CB857D9A551D81BE
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t annotation update)
polyprotein from tr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Embryophyta; Tracheophyta; a; Poales; Poaceae;
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RESULT PLANT OF THE PROPERTY O
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RA LLY Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,

RA LU Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,

RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,

RA Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,

RA Ran S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,

RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,

RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,

RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,

RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,

RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,

RA G.J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;

RI Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BX842602; CAB75882.1; -.

DR GG; GO:0003700; F:transcription factor activity; IEA.

GG; GO:0003700; F:transcription factor activity; IEA.

GG; GO:0003700; F:transcription of transcription, DNA-dependent; IEA.

DR GG; GO:0003700; F:transcription of transcription, DNA-dependent; IEA.

DR GG; GO:0003701; TF_ERF;

DR PRINTS; PR00367; ETHRSPELEMNT.

DR PRINTS; PR00367; ETHRSPELEMNT.

DR SROIENCE 128 Ab: 14193 MW. BRARAPERAB171066 CBC64.
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Best Local S
Matches 17
   Query Match
Best Local
                                                                                                Gong W., Pan Y., Peng X.Y., Yang i Submitted (AUG-2003) to the EMBL/(EMBL; ABA025608; BAA95736.1; -. EMBL; AJS80377; CAE45639.1; -. HSSP, O80337; CGCC.
GO: GO:0005634; C:nucleus; IEA.
GO: GO:0003700; F:transcription fi GO; GO:0003700; F:transcription fi GO; GO:0006355; P:regulation of the Tropic (Conductor) (Conducto
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Q9LTC5;
01-OCT-2000
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clones.";
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Sato S., Nakamura Y.,
Submitted (APR-1999)
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Aagmoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Nicotiana EREBP-3-like protein (Putative ethylene r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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llarity 100.0%;
Conservative 0;
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8.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang J., Zhu Y.X.;
EMBL/GenBank/DDBJ
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Score 17;
Pred. No.
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                                                                                                           5E43AB05E93B4050 CRC64;
                                                                                                                                                                                                                                         factor activity; IEA.
transcription, DNA-dependent; IEA.
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4 bp covered by sixty
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3. 9.8e-08;
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1.1e-07;
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Mizuno S., Sato T.;
Submitted (NOV-2003) to the EMBL/,
EMBL; AB125975; BAD01555.1; -.
GO; GO:000534; C:nucleus; IEA.
GO; GO:0003700; F:transcription f.
GO; GO:0006355; P:regulation of t.
                                                                                                                                                                                                                                                      Q8LDL4
Q8LDL4;
01-OCT-2002
01-OCT-2002
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05-JUL-2004
05-JUL-2004
                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 26, Last samotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Rthylene responsive element binding factor-like.
Arabidopsis thaliana (Mouse-ear cress)
Rukaryota; Viridiplantae; Streptophyta; Embryophyta
Spermatophyta; Magnollophyta; eudicotyledons; core-
eurosids II, Brassicales; Brassicaceae; Arabidopsis
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Q75UJ5;
Submitted (MAR-2002) to (EMBL; AY085939; AAM63150, HSSP; 080337; 2GCC.
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Name=CMe-ERF1;

Cucumis melo (Muskmelon).

Cucumis melo (Muskmelon).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid

eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                     MEDLINE=22088475; PubMed=12093376;
Haas B.J., Volfovsky N., Town C.D., Tro
Feldmann K.A., Flavell R.B., White O.,
"Full-length messenger RNA sequences g:
                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00380; AP2;
SEQUENCE 165 AA;
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Pfam; PF00847; AP2; 1
                                  Brover V., T
Feldmann K.;
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0; Mismatches
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RESULT
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AC Q9,
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DT 05
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DE Tr.
DE el.
GN Nat
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GO; GO:0003700; F:transcription f;
GO; GO:0006355; P:regulation of t;
InterPro; IPR001471; TF ERF.
PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF_ERF; 1.
SWART; SM00380; AP2: 1
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01-JUN-2003
01-JUN-2003
01-MAR-2004
                                                    O9FKG2 PRELIMINARY; PRT; 201 AA.
O9FKG2;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Transcription factor-like protein (Putative ethylelement binding factor).
                                                                                                                                                                                                                                                                                                                                                                MEDLINE-22816770; PubMed=12935902; DOI=10.1016/S0014-5793(03)00757-9;
TOURTHOE B., Sanchez-Ballesta M.T., Jones B., Pesquet E., Regad F.,
Latche A., Pech J.C., Bouzayen M.;
Latche A., Pech J.C., Bouzayen M.;
"New members of the tomato ERF family show specific expression pattern and diverse DNA-binding capacity to the GCC box element.";
FEBS Lett. 550:149-154(2003).
EMBL; AV19270; AA034706.1; -.
HSSP; O80337; 2GCC.
HSSP; O80337; 2GCC.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005359; P:regulation of transcription, DNA-dependent; IEA.
INTERPROPERTY. TERET.
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Arabidopšis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
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ProDom; PD001423; TF_ERF; 1.
SMART; SM00380; AP2; 1.
                                            Name=At5g61590;
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3 (TrEMBLrel. 24, 1
4 (TrEMBLrel. 26, 1
esponse factor 4.
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Q6V5F2;
05-JUL-2004
05-JUL-2004
STRAIN=Circus maximus;

pubMed=14970339; DOI=10.1073/pnas.0305448101;

Piebig A., Kimport R., Preuss D.;

Piebig A., Kimport R., Preuss D.;

"Comparisons of pollen coat genes across Brassicaceae species rapid evolution by repeat expansion and diversification.";

Proc. Natl. Acad. Sci. U.S.A. 101:3286-3291(2004).

EMBL; AY350713; AAR15465.1; -.
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EWBL; AV045968; AAK76642.1; ---
EWBL; AV079321; AAL85052.1; ---
                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosic eurosids II; Brassicales; Brassicaceae; Capsella.
                                                                                                                                                                    AP2 transcription
ORFNames=Cr 7580;
Capsella rubella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural analysis of Arabidopsis thal Sequence features of the regions of 1,36 physically assigned P1 and TAC clones.", DNA Res. 5:203-216(1998).
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ProDom; PD001423; TF_ERF; 1.
SMART; SM00380; AP2; 1.
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription
GO; GO:000375; P:regulation of
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Karlin-Neumann
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Best Local (
                                                                                                   Q6V5B8 PRELIMINARY;
Q6V5B8;
Q5-JUL-2004 (TrEMBLrel. 27, L.
05-JUL-2004 (TrEMBLrel. 27, L.
05-JUL-2004 (TrEMBLrel. 27, L.
APZ transcription factor.
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GO; GO:0003700; F:transcription if
GO; GO:0006355; P:regulation of t:
InterPro; IPR001471; TF ERF.
Pfam; PF00047; AP2; 1.
PRINTS; PR00367; ETHRSPELEMNT.
PRODOm; PD001423; TF ERF; 1.
SMART; SM00380; AP2; 1.
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
AP2 transcription factor/ethylene response element.
ORFNames=Bo_7580;
Brassica oleracea (Cauliflower).
ORFNames=Aal 7580;
Arabidopsis arenosa.
Arabidopsis arenosa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
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SMART; SM00380;
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InterPro; IPRO01471; TF_ERF.
Pfam; PF00847; AP2; 1.
PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF_ERF; 1.
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"Comparisons of pollen coat genes across Brassicaceae species rapid evolution by repeat expansion and diversification.";
Proc. Natl. Acad. Sci. U.S.A. 101:3286-3291(2004).
EMBL; AY350710; AAR13699.1; -.
GOBO005634; Cruncleus; IEA.
GO; GO:0005700; F:transcription factor activity; IEA.
GO; GO:0005700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
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Matches 17
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Pibbig A., Kimport R., Preuss D.;
Piebig A., Kimport R., Preuss D.;
"Comparisons of pollen coat genes across Brassicaceae species reveal rapid evolution by repeat expansion and diversification.";
Proc. Natl. Acad. Sci. U.S.A. 101:3286-3291(2004).

EMBL; AY350715; AAR15499.1; -.
GO; GO:0005534; C:nucleus; IEA.
GO; GO:0005700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; ITR001471; TF_ERP.

DEAM: PF00047; AP2; 1.
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ProDom; PD001423; TF ERF; 1.
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NCBI_TaxID=38785;
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112
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                                                               Similarity
               GVRRRPWGKFAAEIRDP 118
GVRRRPWGKFAAEIRDP
                                                    Conservative
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Search completed: February 27, 2005, 22:26:24 Job time : 176 secs

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BD269586 Method of AX033192 Sequence AJ251240 Catharant CQ808982 Sequence AY088387 Arabidops CQ805290 Sequence AX507520 Sequence AX507520 Sequence AF325089 Arabidops AY072471 Arabidops D38123 Nicotiana t AF370540 Arabidops BD269585 Method of AX033191 Sequence AJ238740 Catharant AF057373 Nicotiana t AF0370740 Catharant AF057373 Nicotiana t AF0370740 Catharant AF057373 Nicotiana t AF057
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ALIGNMENTS

FEATURES source		JOURNAL COMMENT	REFERENCE AUTHORS TITLE	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BD269586 LOCUS DEFINITION
CC cells FH Key Location/Qualifiers FT Source 1792 FT periwinkle)'. Location/Qualifiers 1792 /organism="Catharanthus roseus (madagascar FT periwinkle)'. Location/Qualifiers 1792 /organism="Catharanthus roseus" /mol_type="genomic DNA"	HAN ANC 2N1	BOMEALE CELIS PATENT: JP 2002535993-A 3 29-OCT-2002; RIJKSUNIVERSITEIT LEIDEN OS Catharanthus roseus (madagascar periwinkle) DN JP 2002535993-A/3	Eukaryota; Viridiplantae; Streptopnyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae; Catharanthus. 1 (bases 1 to 792) 1 (bases 1 to 792) Memelink,J., Der,C.T.E.V., Fits, Menke,F.L.H. and Kijne,J.W. Method of modulating biosynthesis of metabolite in recombinant	BD269586 1 G1:33079354 BD269586.1 G1:33079354 Gatharanthus roseus (Madagascar periwinkle) Catharanthus roseus	BD269586 792 bp DNA linear PAT 17-JUL-2003 Method of modulating biosynthesis of metabolite in recombinant

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TTCTGTGAAATGAGAGATTATTACGTGGTTTTTTGTTAAGCCCGATTAATCCCCTCATTGTAA
                                                                     AGTGGAGGAAGGAAGAAGACGATATTAATTAATTAAAAAGTGGAGGATTAAAAAAA
                                                                               CGTTTCCCTGCGGAGCCTTCTACGACGTCGTCGTCTTCTTCTTCTTCTTCGTCTAAAAAT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; seterids; lamiids; Gentianales; Apocynaceae; Rauvolfioideae;

Memelink,J., Kijne,J.W., Menke,F.L. and van omethod of modulating metabolite biosynthesis Patent: WO 0046383-A 3 10-AUG-2000; UNIV LEIDEN (NL); MEMELLNK JOHAN (NL); FITS ELISABE (NL); KIJNE JAN WILLEM (NL); MENKE ; FITS CORNELIA THEODORA MENKE FRANK LEONARDUS der s in Fits, C.T. recombinant cells

/organism="Catharanthus roseus" /mol_type="unassigned DNA" /db_xref="taxon:4058"

h 100.0%; Score 792; DB 6; Similarity 100.0%; Pred. No. 1.1e-205; 92; Conservative 0; Mismatches 0; Length Indels 0, Gaps 0

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AAGGATTGGAACCGGTATAAGGGCGTTAGACGGCGGCGTGGGGGAAGTTCGCGGCGGAG TCTACAGAGGAAAATTGGGAAGAAATTTTTGCAGATTTTCTAAATTGGTCGGGATCCGAA TTCTAAAAAAGAAGAAAATGTCCGAAGAAATCATTTCCGTCTCAGATCGATTTCTTCTT GATGCAGCATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAGGCTT GATGCAGCATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAGGCTT TGTCAGGAGGATTCTGTTGTGGGAACCCCGCCAGAAGCGGCGGCCGGAGGAGGTTGTTCG TGTCAGGAGGATTCTGTTGTGGGAACCCCGCCAGAAGCGGCGGCCGGAGGAGGTTGTTCG ATACAGAAACGCGGTAGCCCGAGTTCCGAAAGCTGTCAATCGAATTCAATGGCGGAAAGC ATACAGAAACGCGGTAGCCCGAGTTCCGAAAGCTGTCAATCGAATTCAATGGCGGAAAGC TCTACAGAGGAAAATTGGGAAGAAATTTTTGCAGATTTTCTAAATTGGTCGGGATCCGAA TCCTTAATCGAAGAACATCTTCTCAGCGATAATTCTGATGATTCCAGCTCGGAATTGACT TCCTTAATCGAAGAACATCTTCTCAGCGATAATTCTGATGATTCCAGCTCGGAATTGACT TTCTAAAAAAGAAGAAAATGTCCGAAGAAATCATTTCCGTCTCAGATCGATTTCTTCTT 180 480 480 420 360 300 240 240 180 120 120 60 420 360 300

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Submitted (25-NOV-1999) Memelink J., Institute of Molecular Plant
Schennes, Leiden University, Wassenaarseweg 64, NL-2333 AL,
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                                                     TCCTTAATCGAAGAACATCTTCTCAGCGATAATTCTGATGATTCCAGCTCGGAATTGACT
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/db_xref="UniProt/TæRBE:Q9LDB6"
/db_xref="UniProt/TæRBE:Q9LDB6"
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/dev_stage="mature_plant"
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/product="AP2-domain_DNA-binding
/protein_id="CAB96899.1"
/db_xref="GI:8980313"
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Direct Submission
Submitted (25-NOV-1999) Memelink J., Institute of Molecular Sciences, Leiden University, Wassenaarseweg 64, NL-2333 AL,
                                              2 (bases 1 to 1816)
Memelink, J.
                                                                                                          van der Fits,L. and Memelink,J.
ORCA3, a jasmonate-responsive transcriptional
primary and secondary metabolism
Science 289 (5477), 295-297 (2000)
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                             GTGGAGGAAGGAAGAGA 621
                                                                                                                                                   ATTTTCCTCATTTGATTGGTTCGAATATTTCCGGACCCGTTAGAGTAAACCCGAGAAAAC
                                                                                                                                                                                                                 ATGCAGCATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAAGCTTA
                                                                                                                                                                                                                                                                                                 TAAGGGATCCGAAAAAGAAAGGATCCAGGATTTGGTTGGGTACATACGAGACACCTGAGG
                                                                                                                                                                                                                                                                                                                                   AAGATTGGAGACGGTACATAGGAGTTAAACGGCGGCCGTGGGGGACGTTTTCGGCGGAGA
                                                                                               GTTTCCCTGCGGAGCCTTCTACGACGTCGTCGTCTTCTTCTTCTTCGTCTGAAAATA
                                                                                                                                ATTTTCCTCACTTAATTGGATCAAACATTCCTAAGCCGGCTAGAGTTACAGCGAG---AC
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                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Nicotiana tabacum"
/mol_type="unassigned DNA"
/db_xref="taxon:4097"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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Pred. No. 3.2e-31;
0; Mismatches 93;
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                                                                                                                                                                                                                                                                                                                                                                                                         CDS
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                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malibu, CA 90265, USA

This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TICR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the considered to be 3'-truncated if it lacks the sequences are derived from the Ws or Lacer ecotypes and therefore may contain polymorphisms when compared to sequencing of the Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the full-length clones. Selection of clones, and sequence assembly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 914)
Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feldmann, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana clone
AY088387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Full-Length cDNA from Arabidopsis thaliana Unpublished
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FLI_CDNA.
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CCGTTACCTCTCCGGCGGAGGAAGATAAGCCTCCGGCGAAGGCGAAGGCGAGTGGCTCACACG 349
                                          CGGAAAGCTGTCAGGAGGATTCTGTTGTGGGAACCCCCGCCAGAAGCGGCGGCCGGAGGAG 292
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                                                                                      Conservative
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                                                                                                                                                                                          RIRPRRRSPEPSVSDQLTSEQKRESHVDDGKSSLVVPELDFTVDQFYFDGSLLMDQSE
CSYSDNRI"
                                                                                                                                                                                                                              /translation="msssdsvningvnsmyfripsfsnvilindnwsdlplsvddsodm
AIYNTLRDAVSSAWTPSVPFVTSPAEEDKPPATKASGSHAPROKGMQYRGVRRPWGK
FAAEIRDPKKNGARVWLGTYETPEDAAVAYDRAAFQLRGSKAKLNFPHLIGSCKKEPV
                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="putative ethylene response element binding
protein (EREBP)"
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="6397"
                                                                                                                                                                                                                                                                                              /protein_id="AAM65925.1"
/db_xref="GI:21594007"
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                                                                                                    17.1%;
64.2%;
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                                                                                  Score 135.6; DB 8;
Pred. No. 7.6e-26;
0; Mismatches 114;
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Identification of novel e2f target genes
Patent: WO 2004035798-A 1701 29-APR-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
roside; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                          CGAGAAAACGTTTCCCTG
                                                                                                          CTAGGCTTAATTTTCCTCATTTGATTGGTTCGAATATTTCCGGACCCGTTAGAGTAAACC
                                                                                                                                                                      CGCCGGAGGACGCGGTGGCGTACGACCGAGCGGCGTTTCAGCTCAGAGGATCGAAAG
                                                                                                                                                                                                     CACCTGAGGATGCAGCATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAG
                                                                                                                                                                                                                                                         CGGCGGAGATTAGGGATCCGAAGAAGAACGGAGCTAGGGTTTGGCTCGGGACTTACGAGA
                                                                                                                                                                                                                                                                                                 CGCCGAGGCAGAAGGGGATGCAGTACAGAGGAGTGAGGAGGAGGCCGTGGGGGAAATTCG
                                                                                                                                                                                                                                                                                                                                                                                     GTTGTTCGAAGGATTGGAACCGGTATAAGGGCGTTAGACGGCGGCCGTGGGGGAAGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                               CCGTTACCTCTCCGGCGGAGGAAAATAAGCCTCCGGCGACGAAGGCGAGTGGCTCACACG
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    CTCGCCGTCGCTCGCCGG
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/mol_type="unassigned [
/db_xref="taxon:3702"
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0; Mismatches 1
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                                        FLI CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

**Tranda,M.,**
**Tr
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Sequence 221
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AX507520.1
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AF325089
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Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                       AF325089.1 FLI_CDNA.
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Arabidopsis thaliana putative ethylene response protein (EREBP) (At2944840) mRNA, complete cds.
                Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Palm, C.J., Theologis, A., Ecker, J. and Davis, R.W.
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/mol_type="unassigned I
/db_xref="taxon:3702"
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JOURNAL
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (Dases 1 to 727)

Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
                                                                                                                                                                                                                                                                                                                                                                 AY072471 727 bp mRNA linear PLN Arabidopsis thaliana putative ethylene response element protein (EREBP) (At2944840; T13E15.15) mRNA, complete co
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                                                                                                                                                                                                                                  Arabidopsis thaliana (thale cress)
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Similarity 63.8%;
03; Conservative
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/db_xref="GI:13272437"
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RIRPRRRSPEPSVSDQLTSEQKRESHVDDGESSLVVPELDFTVDQFYFDGSLLMDQSE
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/product="putative ethylene response
protein (ERESP)"
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/db_xref="taxon:3702"
/clone="c6030"
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Pred. No. 2e-25;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satuu,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen, M., Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M.K., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e-mail for correspondence: arab@sequence.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02-JAN-2002) DNA Sequencing and Technology Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      equally to this work.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nguyen, M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stanford University, 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGAAAGCTGTCAGGAGGATTCTGTTGTGGGAACCCCGCCAGAAGCGGCGGCCGGAGGAG 292
                                                                                                                                                                                                                                                                            CGCCGAGGCAGAAGGGGATGCAGTACAGAGGAGGAGGAGGAGGCCGTGGGGGAAATTCG
                                                                                                                                                                                                                                                                                                                                                                  GTTGTTCGAAGGATTGGAACCGGTATAAGGGCGTTAGACGGCGGCCGTGGGGGAAGTTCG 352
                                                                                                                                                                                                                                                                                                                                                                                                                  CCGTTACCTCTCCGGCGGAGGAAAATAAGCCTCCGGCGACGAAGGCGAGTGGCTCACACG 250
  CGAGAAAACGTTTCCCTG 550
                                               CTAAGCTGAATTTTCCGCATTTGATTGGTTCTTGTAAGTATGAGCCGGTTAGGATTAGGC
                                                                            CTAGGCTTAATTTTCCTCATTTGATTGGTTCGAATATTTCCGGACCCGTTAGAGTAAACC 532
                                                                                                                                        CGCCGGAGGACGCGGCGTTGGCGTACGACCGAGCGGCGTTTCAGCTCAGAGGATCGAAAG
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                                                                                                                                                                                                                                 CGGCGGAGATTAGGGATCCGAAGAAGAACGGAGCTAGGGTTTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAL66886.1"
/db_xref="GI:18377440"
/tzanslation="MSSSDSYUNGVNGRMYFRNPSFSNVILNDNWSDLPLSVDDSQDM
AIYNTLRDAVSSGWTPSVPPVTSPAEENKPPATKASGSHAPRQKGMQYRGVRRPWGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative ethylene
protein (EREBP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAAEIRDPKKNGARVWLGTYETPEDAAVAYDRAAFQLRGSKAKLNFPHLIGSCKYEPV
RIRPRRRSPEPSVSDQLTSEQKRESHVDDGESSLVVPELDFTVDQFYFDGSLLMDQSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed o this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="At2g44840;
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/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 134; DB 8
Pred. No. 2e-25;
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AUTHORS
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Best Local
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TITLE
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288 AGGAGGTTGTTCGAAGGATTGGAACCGGTATAAGGGGGGTTAGACGGCGGCCGTGGGGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bioscience and Human Thechnology, Plant Moplecular Biology
Laboratory; 1-1 Higashi, Tsukuba, Ibaraki 305, Japan
(E-mail:masaru@nibh.go.jp, Tel:0298-54-6071, Fax:0298-54-6095)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suzuki, K., Suzuki, N., Ohme-Takagi, M. and Shinshi, H. Immediate early induction of mRNAs for ethylene-responsive transcription factors in tobacco leaf strips after cutting plant J. 15, 657-665 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohme-Takagi,M. and Shinshi,H.

Ethylene-inducible DNA binding proteins that interact ethylene-responsive element plant Cell 7 (2), 173-182 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence updated (04-Apr-1995) by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERF1; ethylene-responsive transcription factor Nicotiana tabacum (common tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Masaru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-SEP-1994) Masaru Ohme-Takagi, National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohme-Takagi,M.
Direct Submission
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                                                                                                                                       Similarity
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                                                   AAAATCGGAGCAGAGGAAGAAATTGTGGTTTCTCCGGCGGAGACGACGCCGCGCCC
                                                                                AATGGCGGAAAGCTGTCAGGAGGATTCTGTTGTGGGAACCCCGCCAGAAGCGGCGGCCGG
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741. .841
841
                                                                                                                                                                                                                                                            /trānslation="MNQPIYTELPPANFPGEFPVYRRNSSFSRLIPCLTETWGDLPLK
VDDSSDMYIYTLKDALNVGMSPFNFSAGEVKSEGREEEIVVSPAETTAAPAAELPRG
RHYKGVRRRPWGKFPAAEIRDPAKNGARVWLGTYETDEEAAIAYDKAAYRMRGSKAHL
FPHRIGLNBPEPVRVTAKRRASPEPASSSENSSPKRRRKAVATEKSEAVEVESKSNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="leaf"
/clone_lib="lambda ;
/dev_stage="mature"
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/db_xref="GI:1208495"
                                                                                                                                                                                                                                                                                                                                                                     /product="ERF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="ERF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Nicotiana tabacum"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                       note="ethylene-responsive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:4097"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain="BY4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                     16.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          stage="mature"
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mRNA for ERF1,
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                                                                                                                        0
                                                                                                                     Score 134; DB E
Pred. No. 2e-25;
0; Mismatches 1
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                                                                                                                                                        DB 8;
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                                                                                                                        160;
                                                                                                                                                      Length 841;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treated leaf"
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Gaps

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DEFINITION
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                                                                                                                                                   FEATURES
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                                                                                                                                              Nguyen,M., (SSP/Stanford) and Seki,M. (RIKE
equally to this work. Shinozaki,K. (RIKEN
(SSP/Stanford) contributed equally to this
Location/Qualifiers
                                                                                                                                                                                                                                                                     The Salk, Stanford, PGEC (SSP) Consortium members carried out th sequencing and annotation of the RAFL cDNAs: Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAs (RAFL CDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (17-APR-2001) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 887)

Nguyen, M., Karlin-Neumann, G., Southwick, A., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carningi, P., Chen, H., Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Shinnzaki, K., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF370540 887 bp mRNA linear PLN Arabidopsis thaliana putative ethylene response element protein; EREBP (At2g44840; T13E15.15) mRNA, complete cd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e-mail for correspondence: arab@sequence.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF370540.1 GI:13899090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGGAGAAGAAGGCTGTTGCAACTGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCGTCTGAAAATAGTGGAGGAAGGAAGAA 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAACCCGAGAAAACGTTTCCCTGCGGAGCCTTCTACGACGTCGTCGTCTTCTTCTTC 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGGCTCATTTAAATTTTCCCACATAGAATCGGTTTAAATGAACCGGAACCGGTTCGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAAGCTAGGCTTAATTTTCCTCATTTGATTGGTTCGAATATTTCCGGACCCGTTAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAGACACCTGAGGATGCAGCATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTTGCGGCGGAGATTAGGGATCCGGCGAAGAATGGAGCTAGGGTTTGGCTTGGAACATA
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  /clone="RAFL05-13-E10"
/ecotype="Columbia"
                                         /db_xref="taxon:3702"
/chromosome="II"
                                                                                    organism="Arabidopsis/mol_type="mRNA"
                                                                                                                                                                                                                                                      Ecker, J.,
                                                                                                                                                                                                                                                      Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  643
                                                                                                                                                                                                               (RIKEN GSC) contributed
                                                                                                                                                                                          GSC)
                                                                                                                                                                      work as PIs.
                                                                                                                                                                                       and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLN 01-MAY-2001
ent binding
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REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                            REFERENCE
AUTHORS
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AUTHORS
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AC002388/c
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Best Local
                                                                                                       JOURNAL
                                                                                                                             TITLE
                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                            ORGANISM
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Medical Center Dr., Rocky
3 (bases I to 85534)
Town, C.D. and Kaul, S.
Direct Submission
Submitted (27-FEB-2002)
                                                                                                                                                                                                                              1 (bases 1 to 85534)
Rounsley,S.D., Lin,X., Ketchum,K.A.,
Sykes,S.M., Mason,T.M., Kerlavage,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC002388 85534 bp DNA line Arabidopsis thaliana chromosome 2 clone T13E15
                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                       Submitted (09-MAR-2000)
                                                                                                                             Direct Submission
                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                             and Venter, J.C.
                                                                                                                                                                                                                                                                                             rosids; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                        AC002388.3
                                                                                                                                                Lin, X
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                                                                                                                                                                      (bases 1 to 85534)
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RIRPRRRSPEPSVSDQLTSEQKRESHVDDGESSLVVPELDFTVDQFYFDGSLLMDQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; EREBP"
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/product="putative ethylene response element binding
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                                                                                    Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                607
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Pred. No. 2.1e-25;
0; Mismatches 115
    The
                                                                                                       The Institute for Genomic
                                                                                                                                                                                                                                 Kerlavage, A.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is in pBluescript"
    Institute
                                                                                      ₹
                                                                                    20850,
                                                                                                                                                                                                                                 R., Adams, M.D., Somerville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115;
    for Genomic
                                                                                      USA
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589 532 529 472 469 412 409 352 349 292

Research,

9712

Research,

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Somerville, C.R.

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COMMENT
FEATURES
                                                                                                                                                                                                                                                                                                                                           mRNA
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                                                                                                                                                                                                                                                    Sgo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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On Apr 18, 2002 this ---
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6279. .6481)
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SSQMTQTLYNLVAATEDLRCLKDELYPTVLRTNLGKDLCGQLALSELESEIKSFRGDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERQQKLATKID"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="overlap with BAC clone T14P1 (:73419. .89604)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .16186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <5213. .5329,5510. .5671,5752.
.>6481)
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                                                                                                                                                                                                                 142. .8302,8385.
.9498,9591. .947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="AT_rich"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (16897. .16921)
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complement (19422. .19447)
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blprpvtnspkdiqaaaslaannwddsundusnsbuabivbabesravualfessdts
tttttqsqbtss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="At2g44930"
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23937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .21797,21971. .22344,22489. .23336,23444. .23760)
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2. .27182,27295. .27947,28442. .

.27376

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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                RESULT 14
BD269585
LOCUS
                                                                                                                                               ACCESSION
VERSION
                                                                                                                                                                                                            DEFINITION
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Best Local S
Matches 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203;
                 Catharanthus roseus (Madagascar periwinkle)
Catharanthus roseus
Catharanthus roseus
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                         JP 2002535993-A/2.
                                                                                                                                               BD269585
BD269585.1 GI:33079353
                                                                                                                                                                                                          Method of modulating biosynthesis
                                                                                                                                                                                        somatic cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACCTGAGGATGCAGCATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCCGAGGCÁGAAGGGÁTGCAGTACAGAGGAGTGÁGGAGGAGGCCGTGGGGGAAATTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTGTTCGAAGGATTGGAACCGGTATAAGGGCGTTAGACGGCGGCCGTGGGGGAAGTTCG
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                                                                                                                                                                                                                                                                                                                                        CTCGCCGTCGCTCGCCGG
                                                                                                                                                                                                                                                                                                                                                                                 CGAGAAAACGTTTCCCTG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCCGGAGGACGCGGCGGTGGCGTACGACCGAGCGGCGTTTCAGCTCAGAGGATCGAAAG
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Catharanthus.
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complement (29435. .29473)
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/protein_id="AAC31832.2"
/db_xref="GI:20196924"
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/codon_start=1
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               AUTHORS
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Best Local
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Patent: JP 2002535993-A 2 29-OCT-2002;
RIJKSUNIVERSITEIT LEIDEN
OS Catharanthus roseus (madagascar peri PR JP 2002535993-A/2
PD 29-OCT-2002
PF 07-FEB-2000 JP 2000597442
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PR 05-FEB-1999 DK PA 199900158,10-FEB-1999 US 60/119388 PI JOHAN MEMELINK, CORNELIA THEODORA ELISABETH VAN DER FITS, PI FRANCISCUS LEONARDUS HENDRIKUS MENKE, JAN WILLEM KIJNE PC C12N15/09, A01H5/00, C12N5/10, C12P5/00, C12P7/22, C12P13/00, C12P17/
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Memelink,J., Der,C.T.E.V., Fits, Menke,F.L.H. and
Method of modulating biosynthesis of metabolite in
Memelink,J., Kijne,J.W., Menke,F.L. and van omethod of modulating metabolite biosynthesis Patent: WO 0046383-A 2 10-AUG-2000;
                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Gentianales; Apocynaceae; Rauvolfioideae;
                                                                                                                    Catharanthus roseus (Madagascar periwinkle)
                                                                                                                                                                                 Sequence 2 from AX033191
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:4058"
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                                                                                         610 GAT 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Catharanthus roseus"
/mol_type="unassigned DNA"
/db_xref="taxon:4058"
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ADM72374	AAV00614	ADF99632	ADI42014	AD002565	ADK59746	ADJ10797	AAZ50843	AAA53744	AD001614	ADI41542	ADE37188	AAD06444	AAC44305	ABQ65748	ADN73806	ABZ14410	AAC40522	ADF99769	AAA53745	ID	
Adm72374 Soybean N	Aav00614 Lycopersi	Adf99632 Nicotiana	Adi42014 Plant tra	Ado02565 Soybean o	Adk59746 Plant DNA	Adj10797 Recombina	Aaz50843 Tobacco s	Aaa53744 Plant tra	Ado01614 Thalecres	Adi41542 Plant tra	Ade37188 Plant yie	Aad06444 Arabidops	Aac44305 Arabidops	Abq65748 Arabidops	Adn73806 Thale cre	Abz14410 Arabidops	Aac40522 Arabidops	Adf99769 Nicotiana	Aaa53745 Plant tra	Description	

Modulating level of metabolites and stress resistance in recombinant cells for synthesis of plant metabolites such as alkaloids including terpenoid indole alkaloids, by providing transcription factor to the cell.

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Abk65149 Arabidops Acd98367 A. thalia	Aad06475 Arabidops	Ado02581 Soybean o	Adi42030 Plant tra	Ado03418 Thalecres	Ado02256 Thalecres	Adi43610 Plant tra	Acd98375 A. thalia	Abk65330 Arabidops				Þ		A.	Adg87787 A. thalia	Abz12349 Arabidops	Aac47651 Arabidops	Aac34142 Arabidops	. Ado02566 Soybean o	Adi42015 Plant tra	Adm72372 Soybean N	Ado02586 Soybean o	Adi42035 Plant tra

## ALIGNMENTS

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RESULT 1

AAA53745

ID AAA53745 standard; DNA; 792 BP.

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AC AAA53745;

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T 19-DEC-2000 (first entry)

DT 19-DEC-2000 (first entry)

XX

Plant transcription factor; plant metab procession; modulating flavouring; fragrament from the control of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AP2; transcription factor; plant metabolism; metabolite; primary; secondary; alkaloid; terpenoid indole alkaloid; TIA; pharmaceutical; food colouring; flavouring; fragrance; antimicrobial; pathogenic; insecticide; gene expression; modulation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant transcription factor AP2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=  a
/product= "AP2 polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                     Menke FLH,
                                                                                                                                                                                                                                                                                                                                                                                                          Kijne JW;
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CC Many plant secondary metabolites have value as pharmaceuticals, food CC colourings, flavours and fragrances. Some plant secondary metabolites are CI linked to plant or plant cell defence mechanisms and may confer to the CC plant antimicrobial activity, protection against UV light, herbivores, CC pathogens, insects and nematodes. Plant secondary metabolites such as CC terpenoid indole alkaloids (TIA) represent a class of pharmaceutically CC useful compounds which naturally occur in many plant species. New methods CC are described which modulate the expression of one or more genes involved CC in the biosynthesis of plant metabolites or their precursors in plant CC encoding a transcription factor comprises inserving into a plant cell a sequence compounds transcription factor comprising an AP2 DNA-binding domain are useful as central CC pregulators of complex metabolite pathways involving numerous target genes CC for such transcription factors. This means that the yield of commercially CC valuable metabolite compounds can be enhanced and the tolerance of plants CC towards exogenous stress factors can be influenced. The method is useful CC for modulating the level of one or more metabolities. By providing CC by at least 10%, 25% or 100% or reduced 10%, 25%, 50% or 90% relative to CC a cell to which the transcription factor is not provided
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                                                                                                    CGTTTCCCTGCGGAGCCTTCTACGACGTCGTCGTCTTCTTCTTCTTCGTCTGAAAAT
                                                                                                                                                                        AATTTTCCTCATTTGATTGGTTCGAATAITTCCGGACCCGTTAGAGTAAACCCGGAGAAAA
                                                                                                                                                                                                                                                                   GATGCAGCATTGGCTTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAGGCTT
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GATGCAGCATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAGGCTT
                                                                                                                                                                                                                                                                                                                             TCTACAGAGGAAAATTGGGAAGAATTTTTGCAGATTTTCTAAATTGGTCGGGATCCGAA
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Pred. No. 2.8e-205;
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TAAGGGATCCGAAAAAGAAAGGATCCAGGATTTGGTTGGGTACATACGAGACACCTGAGG

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                                                                                                Query Match
Best Local S
Matches 224
                                                                                                                                                                                                                                           The present invention describes an isolated polypeptide that modulates the production of at least one secondary metabolite in an organism, or its derived cell. The polypeptide is selected from a polypeptide encoded by a polynucleotide comprising any of the 871 nucleotide sequences given in the specification. The polypeptides and polynucleotides are useful in modulating the biosynthesis of secondary metabolites (e.g. alkaloids or phemylpropanoids) in an organism or its derived cell. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polypeptides and polynucleotides useful biosynthesis of secondary metabolites (e.g. alkaloids phenylpropanoids) in an organism or its cell.
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(VTTB-)
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04-JUL-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secondary metabolite modulator; biosynthesis; alkaloid; phenylpropanoid; tobacco; Nicotiana tabacum variant bright yellow; Nicotiana tabacum BY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADF99769 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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                                                                                                   Local Sinhes 224;
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                                                                                                                          Similarity
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  AAGATTGGAGACGTACATAGGAGTTAAACGGCGGCCGTGGGGGACGTTTTCGGCGGAGA
                                               AGGATTGGAACCGGTATAAGGGCGTTAGACGGCGGCGGCGGGGGAAGTTCGCGGCGGAGA
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                                                                                                                                                                                                    BP;
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2002EP-00077674
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0; Mismatches
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Matches 204;
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26-JAN-2001;
22-JUN-2001;
The invention relates to identifying a stress condition to which a cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleis in the plant cell with array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell
                                                                                                    Claim
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29-OCT-1999;
                                                                                                                                 Identifying a stress condition to which a producing plants with increased tolerance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene; ss; plant; transgenic; E2Fa/DPa transcription factor;
growth regulator; animal feed product; thale cress;
cell wall biosynthesis; nitrogen metabolism; carbon metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
Altering plant characteristics, useful for producing plants for enzyme pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004035798-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                         18-OCT-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-2004
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)B; ADN73807.
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Pred. No. 4.8e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a novel method for altering one or more plant CC characteristics. Specifically, it refers to identifying genes that are up CC - or down-regulated in transgenic plants overexpressing the heterodimeric CC EZFA/DPA transcription factor of Arabidopsis and using these sequences to calter plant characteristics accordingly. The present invention describes CC generating transgenic plants for the production of growth regulators, cc enzymes, therapeutics, pharmaceuticals and animal feed products, where CC the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture cror physiology, altered endoreduplication, biochemistry, signal cransduction, storage lipid mobilisation and/or altered photosynthesis, ceach relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers companies can also be useful as positive or negative selectable markers companies can also be useful as positive or negative selectable markers could transformation of cells or tissues. The identified genes play a companie transformation feels or transcription factors. This polymucleotide sequence is thale cress cDNA repressed 1.3 fold or more in plants overexpressing the E2Fa/DPa cranscription factor, given in an exemplification of the invention.
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Best Local :
                                                                                                             Arabidopsis thaliana; thale stress; metabolic pathway; k
                                                      Arabidopsis
                                                                                                                                                                 Arabidopsis thaliana
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                                                                                     ana; thale cress; plant; transgenic; GMO; (
pathway; biosynthetic pathway; nutrition;
biotic; ds.
                                                                                                                                                                                                                                                                                 DNA;
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                                                                                                                                                                   polynucleotide SEQ ID NO
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Pred. No. 4.8e-26;
0; Mismatches 115
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                                                                                                         fungicide;
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Matches 203
                                                                                                                                                                                                                                                     fragments. (I) are used to express the corresponding polypeptides (II) or to produce genetically modified plant cells or transgenic plants, which may have improved resistance to disease or stress, or altered metabolic/biosynthetic pathways (for production of commercial, nutritional or medicinal products), or generally any trait of interest, or can be used to screen for biologically active agents (e.g. fungicides, insecticides and antibiotics). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO at sequence.html?DocID=999909770149
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Rameaka
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Hurban
                                                                                                                                                                                                                                                                                                                                                                           The invention relates to nucleic acids (I) that hybridise under stringent conditions to any of 999 sequences (ABQ65424-ABQ66422) or their
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                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
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les 203; Conserv
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SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
HURBAN P.
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PAGE A.

WATHEW A V.

LEDFORD B L.

WOESSNER J P.

HAAS W D.

GARCIA C A.
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                                                                                                                                       CCGTTACCTCTCCGGCGGAGGAAAATAAGCCTCCGGCGACGAAGGCGAGTGGCTCACACG
                                                                                                                                                         SEQ ID NO 325;
              CACCTGAGGATGCAGCATTGGCTTAATGCAGCCGCGTTTAATATGCGTGGAGCTAAAG
                                          CGGCGGAGATTAGGGATCCGAAGAAGAACGGAGCTAGGGTTTTGGCTCGGGACTTACGAGA
                                                          CGCCGAGGCAGAAGGGATGCAGTACAGAGGAGTGAGGAGGAGGCCGTGGGGGAAATTCG
                                                                                                              GTTGTTCGAAGGATTGGAACCGGTATAAGGGCGTTAGACGGCGGCCGTGGGGGAAGTTCG
                                                                                                                                                                                                                                  685 BP; 171
CGCCGGAGGACGCGGCGGTGGCGTACGACCGAGCGGCGTTTCAGCTCAGAGGATCGAAAG
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, Page A, M
Kricker M,
                                                                                                                                                                                      Conservative
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A, Mathew AV,
Pr M, Slater T,
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                                                                                                                                                                                    Score 134; DB 6; I
Pred. No. 4.8e-26;
0; Mismatches 115;
                                                                                                                                                                                                                                  202 G; 173 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence Listing; English.
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Ledford BL,
Loavis KR, J
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BL, Woessner
R, Allen K,
                                                                                                                                                                                                        Length 685;
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JP, Haas !
Hoffman N;
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30-APR 1999
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11-MAY 1999
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99US-0130510P
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99US-0132484P
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99US-0132487
99US-013421863P
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99US-0128234P.
99US-0128714P.
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                                                                            Query Match 16.9%;
Best Local Similarity 63.8%;
Matches 203; Conservative
                                                                         11-AUG-1999
11-AUG-1999
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233 CGGAAAGCTGTCAGGAGGATTCTGTTGTGGGAACCCCGCCAGAAGCGGCGGCCGGAGGAG
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S-015695P.
S-016698P.
S-016136P.
S-016139P.
S
                               Score 134; DB 3; 1
Pred. No. 5e-26;
0; Mismatches 115;
                                                  Length
                                 Indels
                                                       781;
                                0;
                                 Gaps
             292
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10-UN-1999
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99US-0113847P
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RESULT 8
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Reuber
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                                        Nucleic acids encoding plant transcription facto
                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-NOV-1999;
17-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                               (MEND-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-NOV-2000; 2000WO-US031458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-AUG-2000;
                                                                                                                                                                                                                                              (KEDD/)
                                                                                                            2001-336000/35.
DB; AAE02464.
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                                                                                                                                                                                                                                                                PINEDA O.

YU G.

CREELMAN R.

RIECHMANN J L.

HEARD J.

RATCLIFFE O.

REUBER L.
                                                                                                                                                                            Ļ0
                                                                                                                                                                                                                                                                                                                                                                                               MENDEL BIOTECHNOLOGY INC PINEDA O.
                                                                                                                                                                                                                                              KEDDIE
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2000US-0227439P.
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/product= "Arabidopsis thaliana
                                                                                                                                                                              Creelman
; J;
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                                           factor polypeptides, rance characteristics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modifying a plant's phenotype in desirable ways, such as modifying a plant such as modifying a conditying a plant such as the transcription factor is encoded by environmental stress tolerance gene derived from Arabidopsis thaliana. The transcription factors and the genes encoding them are used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, onion, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas. These sequences tolerance, such as freezing, chilling, heat, drought, water saturation, salt, photoconditions, radiation and ozone. The transcription factors are sequences and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 203; Conserv
                                                                                                    ds; gene; transcription factor; tolerance; environmental condition; microbial disease; fungal disease; viral disease; pest infestation; herbicide sensitivity; heavy metal tolerance; heavy metal uptake; growth improvement; photocondition; nutrient uptake; hormone sensititransgenic plant.
                             CDS
                                                                                                                                                                                                   Plant yield
                                                                                                                                                                                                                                                                                              ADE37188 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 913 BP; 249
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                                                                          Arabidopsis
                                                                                                                                                                                                                                    29-JAN-2004
                                                                                                                                                                                                                                                                 ADE37188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence is a cDNA encoding Arabidopsis thaliana nscription factor. This novel transcription factor is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 CGGAAAGCTGTCAGGAGGATTCTGTTGTGGGAACCCCGCCAGAAGCGGCGGCGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACCTGAGGATGCAGCATTGGCTTATGATGCAGCCGCGTTTAATATATGCGTGGAGCTAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGAGAAAACGTTTCCCTG
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                                                                            thaliana
                                                                                                                                                                                                     related
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                             Location/Qualifiers 81. .761
                                                                                                                                                                                                                                                                                                cDNA;
                                                                                                                                                                                                     polynucleotide clone G22.
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Pred. No. 5.4e-
0; Mismatches
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No. 5.4e-26;
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Best Local Similarity
Matches 203; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a number of cDNA sequence and their encoded proteins which are especially transcription factor cDNAs and their proteins. The isolated or recombinant polynucleotide is useful for producing a modified plant with a modified trait, e.g. enhanced tolerance to environmental conditions, improved tolerance to microbial, fungal or viral diseases, improved tolerance to pest infestation, decreased herbicide sensitivity, improved tolerance of heavy metals, or enhanced ability to take up heavy metals, improved growth under poor photoconditions, improved nutrient uptake, or reduced hormone sensitivity. The transgenic plants are useful for growing a progeny plant comprising the desired trait. The polynucleotides and polypeptides are also useful in bioinformatic search methods. This sequence represents one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New stress-related transcription factor polynucleotides and polypeptides, useful for producing transgenic plants with e.g. improved tolerance to diseases or pests, decreased herbicide sensitivity, or improved nutrient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001; 2001US-0310847P.
19-NOV-2001; 2001US-0336049P.
11-DEC-2001; 2001US-0338692P.
14-JUN-2002; 2002US-00171468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reuber TL, | Ratcliffe O,
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 913 BP; 249
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                                                                                                                                 CACCTGAGGATGCAGCATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAG
                                                                                                                                                                                          GTTGTTCGAAGGATTGGAACCGGTATAAGGGCGTTAGACGGCGGCCGTGGGGGAAGTTCG
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                             CGAGAAAACGTTTCCCTG
                                                                                                                                                                                                                                CGCCGAGGCAGAAGGGGATGCAGTACAGAGGAGGAGGAGGAGGCCGTGGGGGAAAATTCG
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 CICGCCGICGCICGCCGG
                                                        CTAAGCTGAATTTTCCGCATTTGATTGGTTCTTGTAAGTATGAGCCGGTTAGGATTAGGC
                                                                                    CTAGGCTTAATTTTCCTCATTTGATTGGTTCGAATATTTCCGGACCCCGTTAGAGTAAACC
                                                                                                                                                                        CGGCGGAGATTAGGGATCCGAAGAAGAACGGAGCTAGGGTTTGGCTCGGGACTTACGAGA
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Pred. No. 5.4e-26;
0; Mismatches 115;
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m PE;
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RESULT 10

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Sherman BK, F
       The invention describes a transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences fully defined in the specification or its complement. The method of the invention can be used to produced a plant having altered traits such as: enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity, disease resistance; sugar sensing; early or late flowering; altered flower structure, change in stem bifurcations, altered branching pattern, reduced apical dominance, reduced trichome trichomes; reduced ectopic trichome development; altered trichome development; increase in trichome number; altered stem morphology; increased root growth; increased root hairs; altered seed development; increased root growth; increased noot hairs; altered seed development; altered cell proliferation or cell differentiation; rapid development; increased in seed morphology; seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; flowering; flower structure; stem bifurcation; branching pattern; apical dominance; trichome; stem morphology; root growth; root hair; seed development; cell proliferation; cell differentiation; premature senescence; necrosis; plant size; leaf morphology; seed morphology; seed biochemistry; root anthocyanin; plant anthocyanin; light response; shade avoidance; bioinformatic;
                                                                                                                                                                                                                                                              New transgenic plant comprising a recombinant of more than 500 nucleotide sequences, useful
                                                                                                                                                                                                                                                                                                        WPI; 2004-132245/13.
P-PSDB; ADI41543.
                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                  methods
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(RIEC/)
(JIAN/)
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                                                                                                                                                                                                                                                                                                                                                                                                         (YUGG/)
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REUBER T L.
KEDDIE J.
BROUN P E.
PILGRIM M L.
DUBELL A N.
PINEDA O.
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CREELMAN R A.
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1, Ratcliffe O, Adam LJ,
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Adam LJ,
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Reuber TL,
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Keddie
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Best Local S
Matches 203
13-SEP-1999;
21-JAN-2000;
17-FEB-2000;
22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
                                                                                                                                                                                                           meristem cell differentiation; phyllotaxy; apical dominance; trichome development; seed development; premature senescence; delayed senescence; lethality; necrosis; plant size; leaf morphology; seed morphology; secondary metabolism; light response; shade avoidanc
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bioinformatic se
factor that can
                                                                                                                                                                                                                                                         Thalecress; transcription factor; ss; gene; plant; transgenic; abiotic stress; cold tolerance; heat tolerance; drought; osmotic phosphate limitation; potessium limitation; nitrogen limitation; hormone sensitivity; disease resistance; sugar sensing; seed germ flowering; inflorescence architectural change;
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                                                                                                            10-APR-2003;
                                                                                                                                                                                     Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                        ADO01614;
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                                                                                                                                                                                                                                                                                                                                       transcription
         99US-00394519
2000US-00489376
2000US-00506720
2000US-00532591
2000US-00533029
2000US-00533039
2000US-005333392
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16-NOV-2000;
27-MAR-2001;
17-APR-2001;
30-JAN-2002;
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Pineda O Pilgrim Sherman 7 J, ₽K, Fromm ME, Reuber TL, Creelman Heard JE, R , Keddie JS, RA, Dubell AN, Riechmann JL, S, Yu G, Jia Yu G, Jiang ( AN, Ratcliffe Adam LJ, °, c Samaha RS; Kumimoto Broun PE; æ

WPI; 2004-225755/21. DB; ADO01615.

New transgenic plant, useful in developing improved characteristics or traits. phenotypes with altered ö

Claim 1; SEQ ID NO 27; 213pp; English

The invention relates to a transgenic plant comprises a recombinant CC polynucleotide having a polynucleotide sequence or its complementary CC sequence comprising a sequence encoding a polypeptide, that initiates CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean, CC Rice, Rape or Corn, comprising any of the sequences appearing as ADO01588 CC -ADO03527 or ADO03520-ADO03559. Also included are using a transgenic CC plant to grow a progeny plant, an expression cassette (comprising a cc constitutive, inducible or tissue-specific promoter and a recombinant CC polynucleotide described above), a host cell comprising the expression CC cassette, producing a modified plant having a modified trait, identifying a factor that is modulated by or interacts with a polypeptide encoded by the polynucleotide sequence that is subject to a regulatory effect of any of CC transgenic plant is useful for producing a plant that has an altered CC transgenic plant is useful for producing a plant that has an altered consistive constitution, forezing tolerance to heat, tolerance to daiootic stress (increased tolerance to heat, tolerance to daiootic stress (increased tolerance to heat, tolerance to obsophate limitation, tolerance to potassium CC limitation, decreased sensitivity to nitrogen limitation, altered susceptibility to Fusarium, altered susceptibility to Sclerotinia, altered susceptibility to Sclerotinia, altered susceptibility to Guiferentiation altered susceptibility to Fusarium, altered susceptibility to Sclerotinia, altered susceptibility to Fusarium, altered susceptibility to Fusarium and Fusarium and Fusarium and Fus altered phyllotaxy, altered branching identifying as ADO01588 tolerance extended

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Best Local Similarity
Matches 203; Conserv
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                                                                                          Catharanthus
                                                                                                                                    AP2; transcription factor; plant metabolism; metabolite; primary; secondary; alkaloid; terpenoid indole alkaloid; TIA; pharmaceutical; food colouring; flavouring; fragrance; antimicrobial; pathogenic; insecticide; gene expression; modulation; ds.
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                      Location/Qualifiers
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                                                                                                                                                                                                                                                       factor AP2 domain.
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63.8%;
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Pred. No. 5.4e-26;
0; Mismatches 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                 pathogens, insects and nematicles. Plant secondary metabolites such as C terpenoid indole alkaloids (TIA) represent a class of pharmaceutically cuseful compounds which naturally occur in many plant species. New methods are described which modulate the expression of one or more genes involved in the biosynthesis of plant metabolites or their precursors in plant cells. The method comprises inserting into a plant cell a sequence encoding a transcription factor comprising an AP2 DNA-binding domain and by modifying the expression of that transcription factor. Transcription factors comprising an AP2 DNA-binding domain are useful as central cregulators of complex metabolite pathways involving numerous target genes for such transcription factors. This means that the yield of commercially valuable metabolite compounds can be enhanced and the tolerance of plants to the acogenous stress factors can be influenced. The method is useful correction factor to the cell the level of the metabolite is enhanced by at least 10%, 25% or 100% or reduced 10%, 25% or 90% relative to
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Sim
Matches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Many plant secondary metabolites have value as pharmaceuticals, food colourings, flavours and fragrances. Some plant secondary metabolites in the linked to plant or plant cell defence mechanisms and may confer to the plant antimicrobial activity, protection against UV light, herbivores,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulating level of metabolites and stress resistance in recombinant cells for synthesis of plant metabolites such as alkaloids including terpenoid indole alkaloids, by providing transcription factor to the
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 885 BP; 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                a cell to which the transcription factor is not provided
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10-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                        ATTTTCCCAATCTTATTGGTTCTGCTAAT---GCTCCGGTTAGAGTAAGTCCTAGACGCC
                                                             ATTTTCCTCATTTGATTGGTTCGAATATTTCCGGACCCGTTAGAGTAAACCCGAGAAAAC
                                                                                                              ATGCGGCATTAGCTTTCGATCAAGCGGCGTTTCAACTCCGTGGTTCTAGAGCTAGGTTAA
                                                                                                                                       ATGCAGCATTGGCTTATGATGCAGCCGCGTTTAATATGTGCGTGGAGCTAAAAGCTAGGCTTA
                                                                                                                                                                                   TCAGGGATCCCAAGAGAAAAGGATCGAGGATATGGTTGGGAACTTACGAGACGGCGGAAG
                                                                                                                                                                                                                      TAAGGGATCCGAAAAAGAAAGGATCCAGGATTTGGTTGGGTACATACGAGACACCTGAGG
                                                                                                                                                                                                                                                            AGGAATGGATTAGGTACCGTGGCGTTIAGACGGCGGCCATGGGGGAAATTCGCTGCGGAAA
                                                                                                                                                                                                                                                                                                                                      Conservative
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99US-0119388P
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                                                                                                                                                                                                                                                                                                                                                   16.7%;
74.5%;
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Pred. No. 1.3
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The patent discloses fifteen new salicylic acid (SA) inducible genes in Nicotiana tabacum, which were identified by differential display PCR. Nine of these genes were subcloned and sequenced. Based on different kinetics of induction response, these genes were classified into four categories, class I, II, III and IV response genes. The SA-inducible genes are useful for making transgenic plants with enhanced pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ50843 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                           resistance. The plants incorporating these genes show reduced susceptibility to fungal pathogens. The present sequence is a specifically claimed SA-inducible gene C18-1 from N. tabacum, belongs to class I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel salicylic acid inducible genes from tobacco plants, useful making transgenic plants with enhanced pathogenic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tobacco plant; salicylic acid inducible gene; SA-inducible gene; transgenic plant; pathogen
                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-1999;
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nes 210; Conserv
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                                                                                                                                                                                                        GGGGAAGGCATTACAGAGGTGTTAGACGACGGCCTTGGGGGAAATTTGCGGCGGAGATTA
                                                                                                                                                                                                                                    ATTGGAACCGGTATAAGGGCGTTAGACGGCGGCCGTGGGGGAAGTTCGCGGCGGAGATAA
                                                                                        GCTGCAATTGCTTATGATAAAGCCGCTTATAGAATGCGTGGTTCAAAGGCTCATTTAAAT
                                                                                                                                                 GGGATCCGGCGAAGAATGGAGCTAGGGTTTTGGCTTGGAACATACGAAACAGATGAAGAT
                                                                                                                                                                       GGGATCCGAAAAAGAAAGGATCCA-GGATTTGGTTGGGTACATACGAGACACCTGAGGAT 423
                                                                                                                                                                                                                                                                                          AGGAGGATTCTGTTGTGGGAACCCCGCCAGAAGCGGCGGCCGGAGGAGGTTGTTCGAAGG
   TTCCCTGCGGAGCCTTCTACGACGTCG
                               TTTCCACATAGGATCGGTTTAAATGAACCGGAACCGGTTCGAGTTACGGCGAAAAGACGA 444
                                                          TTTCCTCATTTGATTGGTTCGAATATTTCCGGACCCGTTAGAGTAAACCCGAGAAAACGT 543
                                                                                                                GCAGCATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAGGCTTAAT
                                                                                                                                                                                                                                                                 AGGAGGAAATTGTGGTTTCTCCAGCGGATACAACGGCCGCCGCCGGCGGCTGAGTTACCGA
                                                                                                                                                                                                                                                                                                                                                                               708 BP;
                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                      16.3%;
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                                                                                                                                                                                                                                                                                                                          116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fungal pathogen;
resistance; C18-1 gene;
                                                                                                                                                                                                                                                                                                                                                    Length 708;
                                                                                                                                                                                                                                                                                                                                                                                  0 Other;
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RESULT 14
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                                                                                                                  Matches
                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                           can be used to generate transgenic plants that are resistant to bacterial speck disease and furthermore exhibit increased resistance against biotic and abiotic stresses. This polynucleotide sequence is a recombinant tomato polynucleotide used to generate genetically engineered, disease resistant plants of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to a method of generating novel genetically engineered plants. Specifically, it refers to compositions useful for transforming plants with a recombinant polynucleotide or plant gene that shows a specific pattern of expression associated with the Avr-Pto mediated defence response. Avr-Pto is described as the avirulent Pto gene found in Pseudomonas syringae pathovar tomato strain [strain T1(A)], which mediates bacterial speck disease in tomato plants. The present which mediates bacterial speck disease in tomato plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New genetically engineered plant comprising a recombinant polynucleotide showing expression associated with Avr-Pto mediated defense response, useful in increasing resistance of plant against bacterial speck disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ10797
                                                                                                                                                                                                                                                                                                                                                                                                                        invention describes identifying genes that are up- or down- regulated the defence response and that are involved in the interaction of Avr-P with Pto and/ or Prf. As such, these novel recombinant polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MYSO/)
(CRAS/)
(FOLK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon esculentum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUN-2004
                                                                                                                                                                                                                            Sequence 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JAN-2002; 2002US-0348792P.
20-JUN-2002; 2002US-0390249P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genetically engineered; plant; Avr-Pto; avirulent Pto;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacterial speck disease; tomato; transgenic; biotic; abiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MART/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2004-081759/08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; SEQ ID NO 193; 176pp; English.
  10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) MARTIN G B
) MYSORE K K
) CRASTA O R
) FOLKERTS O
SWIRSKY P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB,
                                                                                                                                            Similarity
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  TATAGAGGCGTTAGACAGCGTCCGTGGGGGAAATTTGCGGCGGAGATTAGAGATCCGGCG
                                   TATAAGGGCGTTAGACGGCGGCGGGGGGGAAGTTCGCGGGGGGAGATAAGGGATCCGAAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mysore
                                                                                                                  Conservative
                                                                                                                                                                                                                            BP; 140 A; 79 C; 123 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2003US-00341961
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                                                                                                                                         16.2%;
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                                                                                                                                            Score 128.6;
Pred. No. 1.:
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                                                                                                                  Mismatches
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                                                                                                                                                                                                                                  T; 0 U; 0 Other;
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                                                                                                                     79;
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                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or down- regulated in
interaction of Avr-Pto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SeqID
                                                                                                                  <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stress; ds;
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pto gene
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AAGAAAGGATCCAGGATTTGGTTGGGTACATACGAGACACCTGAGGATGCAGCATTGGCT

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RESULT 15
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                                                                                                                                                                                                      The invention comprises DNA sequences which confer an altered metabolic characteristic when they are expressed in a plant. The DNA sequences of the invention are useful for producing plants with an altered metabolic characteristic, such as: altered acid metabolism, alcohol metabolism, fatty acid metabolism, branched fatty acid metabolism, alkaloid or other base metabolism, altered amino acid metabolism, altered ester metabolism, altered metabolism, altered phenolic metabolism, altered carbohydrate metabolism, altered sterol, oxygenated terpene, or isoprenoid metabolism, altered sterol, oxygenated terpene, or oxygenated terpene, or oxygenated terpene, oxygenated terpen
                                                                                                       metabolism, ketone or quinone metabolism. The DNA sequences of the invention may be used to provide disease resistance in a plant and shuffling or sexual PCR procedures. The present nucleic acid represent and the present nucleic acid represent nucleic acid represents nucleic nucleic acid represents nucleic acid represents nucleic acid represents nucleic nucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 7129; 2576pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel genes that confer altered metabolic characteristics in Nicotiana benthamiana plants, useful for altering the levels of metabolites e.g. acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       altered metabolic characteristic; plant; acid metabo alcohol metabolism; fatty acid metabolism; branched fatty acid metabolism; alkaloid metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-313091/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oriedo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADK59746 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-AUG-2001; 2001US-0316471P
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CCGTTAGAGTAAACCCGAGAA                         CCGTTCGAGTTACGGCGAAAA	TGCGTGGAGCTAAAGCTAGGCTTAATTTTCCTGAATTTTGGTTCGAATATTTCCGGAC 	TGGGTACATACGAGACACCTGAGGATGCAGCATTGGCTTATGATGCAGCCGCGTTTAATA 	CGTGGGGGAAGTTCGCGGCGGAGATAAGGGATCCGAAAAAGAAAG	CGGCGGCCGGAGGAGTTGTTCGAAAGGATTGGAACCGGTATAAGGGGGGTTAGACGGCGGC 	14. 67. vative	ion US  ssearcl GENES 4-371  1-371  NUMBER 1997-01 1997-01 1997-01 1997-01 1997-01 1997-01 1997-01 1997-01		1437 1437 1437 1437 1437 1437 1437 1236 326	331 1513 1513 523 530
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		(C)	AGG AGA	AAAT	re 116. d. No. Mismatc	n DISEASE 2,161B 0382	NME	62321111	44004
	0 	\$ _ \$	GATO	TGG#	2.8 ches	ASE	NTS	161B-6 7313-3 7313-3 211A-4 211A-1 211A-1 211A-2 666A-3 217-3 217-3 211A-1 211A-1	211A- 666A- 67-9 211A- 211A-
	ATT	CAGCATTGGC	(2)—(3) (4)—(3)	ACO GAC	рв е-2	RES		3-6 3-6 1-466 1-170 1-127 1-220 1-3 1-3 1-161 1-161	1-176 1-9 1-169
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	517 550	457 491	397 431	337 371	ь			Application of the property of	Ap Ap Ap

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APPLICANT: Pilgrim, Marsha
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Hander, Lynne
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-010
CURRENT APPLICATION NUMBER: US/09/533,029
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PATENTIN OF 2.1
SEQ ID NO 33
LENGTH: 913
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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US-09-533-029-17
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; OTHER INFORMATION: G1006
US-09-533-029-33
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APPLICANT: Keddie, James
APPLICANT: Pineda, Omaira
APPLICANT: Adam, Luc
APPLICANT: Samaha, Raymond
APPLICANT: Stamaha, Raymond
                                                                                                                                                                                           Patent No. 6664446
GENERAL INFORMATION:
                                                                                                                                                                                                                                Sequence 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                     APPLICANT:
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                                                                          APPLICANT: Riechmann, Jose-Luis
APPLICANT: Keddie, James
APPLICANT: Pineda, Omaira
APPLICANT: Adam, Luc
                                                                                                                                                    APPLICANT: Heard, Jacqueline APPLICANT: Brown, Pierre
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APPLICANT: Broun, Pierre
     APPLICANT
                       APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 GAACCGGTATAAGGGCGTTAGACGGCGGCGGCCGTGGGGGAAGTTCGCCGGCGGAGATAAGGGA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 GAAGCATTACAGAGGAGTGAGGCAGAGACCGTGGGGGAAATTCGCGGGGGAGATACGTGA 452
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Samaha, Raymond
Zhang, James
Yu, Guo-Liang
Ratcliffe, Oliver
                                                                                                                                                                                                                                                                                                                            GTCGTCGTCGTCGTCCTCTTCTACGTCGTCGTCT
                                                                                                                                                                                                                                                                                                                                                             TGCGGAGCCTTCTACGACGTCGTCGTCTTCTTCTTCT 585
                                                                                                                                                                                                                                                                                                                                                                                                                                      TCATTTGATTGGTTCGAATATTTCCCGGACCCCGTTAGAGTAAACCCCGAGAAAAACGTTTCCC 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTAGCTTACGATATAGCTGCTTTTAGGATGCGTGGTTCCCGCGCTTTATTGAATTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAGGCTTAATTTTCC 488
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Ratcliffe, Oliver
                                                                                                                                                                                                                                                                                                                                                                                                   GTTGAGGGTTAATTCCGGTGAACCTGACCCGGTTCGGATCACGTCTAAGAGATCTTCTTC
                                                                                                                                                                                                                                Application US/09533029
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Pred. No. 1.3e-22;
0; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104; Indels
                                                                                                                                                                                                                                                                                                                          669
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                                                                                                                     SOPTWARE: ASCII
SEQ ID NO 19
LENGTH: 177
TYPE: DNA
RCANISM: Lycopersicon esculentum
US-09-202-161B-19
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                                                                                                                                                                                                                                                             FILE REFERENCE: 7024-371

CURRENT APPLICATION NUMBER: US/09/202,161B

CURRENT FILING DATE: 1999-06-14

PRIOR APPLICATION UMBER: PCT/US97/10382

PRIOR FILING DATE: 1997-06-12

PRIOR APPLICATION NUMBER: 60/046,494

PRIOR APPLICATION NUMBER: 60/019,633

PRIOR FILING DATE: 1997-05-14

PRIOR APPLICATION NUMBER: 60/019,633

PRIOR FILING DATE: 1996-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Purdue Research Foundation
TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/09202161B Patent No. 6653533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.1%;
Best Local Similarity 63.8%;
Matches 157; Conservative
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                                         Matches
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CURRENT APPLICATION NUMBER: US/09/533,029
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER FILING DATE: 199-03-23
NUMBER OF SEQ ID NOS: 121
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pilgrim, Marsha
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Reuber, Lynne
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             487 CGGCGAAGGGAAAGCATTATAGAGGAGTGAGACAAAGGCCGTGGGGGAAATTTGCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 CGAAGGATTGGAACCGGTATAAGGGCGTTAGACGGCGGCCGTGGGGGAAGTTCGCGGCGG
                                       129; Conservative
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                                                          13.0%;
                                   Score 102.6; DB 4;
Pred. No. 1.3e-20;
0; Mismatches 44;
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Pred. No. 1.6e-20;
0; Mismatches 89;
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                                                                             Length 177;
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US-09-202-161B-20
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US-09-202-161B-5
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; ORGANISM: Lycopersicon esculentum
US-09-202-1618-20
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SOFTWARE: ASCII
SEQ ID NO 5
LENGTH: 761
                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Purdue Research Foundation
TITLE OF INVENTION: GENES ENHANCING DISEASE
FILE REFERENCE: 7024-371
                                                                                                                                                                                                                                                                                          sequence 5, Application US/09202161B
Patent No. 6653533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 119; Conserv
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SOFTWARE: ASCII
SEQ ID NO 20
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                                                                                                             CURRENT APPLICATION NUMBER: US/09/202,161B
CURRENT FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: PCT/US97/10382
PRIOR FILING DATE: 1997-06-12
PRIOR APPLICATION NUMBER: 60/046,494
PRIOR FILING DATE: 1997-05-14
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CURRENT FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: PCT/US97/10382
PRIOR FILING DATE: 1997-06-12
PRIOR APPLICATION NUMBER: 60/046,494
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PRIOR APPLICATION NUMBER: 60/019,633
PRIOR FILING DATE: 1996-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Purdue Research Foundation TITLE OF INVENTION: GENES ENHANCING DISEASE FILE REFERENCE: 7024-371
                                                        PRIOR APPLICATION NUMBER: 60/019,633
PRIOR FILING DATE: 1996-06-12
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 TATAAGGGCGTTAGACGGCGGCCCGTGGGGGAAGTTCGCGGGGGAGATAAGGGATCCGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                            436 TATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAGGCTTAATTTTCC 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 86.6; DB 4;
Pred. No. 7.5e-16;
                                                                                                                                                                                                                                          RESISTANCE
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                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                  Sequence 11, Appli
Patent No. 6664446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                     APPLICANT: Heard, Jacqueline
APPLICANT: Broun, Pierre
APPLICANT: Riechmann, Jose-Luis
APPLICANT: Keddie, James
APPLICANT: Pineda, Omaira
                                         APPLICANT:
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RESULT 7
US-09-640-211A-1401/c
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; ORGANISM: Eucalyptus
US-09-640-211A-1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Lycopersicon esculentum US-09-202-1618-5
US-09-533-029-11
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                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Modification of Gene Transcription FILE REFERENCE: 11000.1021C1U CURRENT APPLICATION NUMBER: US/09/640,211A CURRENT FILING DATE: 2000-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 2368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
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                                                                                        360 CCGCGCCGCGTTCAGGCTCCGCGGGAGCAAGGCCATCCTGAACTTCCCGC
                                                                                                                               441 TGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAGGCTTAATTTTCCTC
                                                                                                                                                                                                            381 AGGATCCAGGATTTGGTTTGGGTACATACGAGACACCTGAGGGATGCAGCATTGGCTTATGA
                                                                                                                                                                                                                                                                 480 GGGCGTGCGCCGGCCGTGGGGGAAGTTCGCGGCGAGATACGCGACCCGACGCGCAA
                                                                                                                                                                                                                                                                                            321 GGGCGTTAGACGGCGGCGTGGGGGAAGTTCGCGGGGGAGATAAGGGATCCGAAAAAAGAA
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Similarity 68.8%;
                                                                                                                                                                            GGGGACGCGTGTGGCTGGGGACGTTCGACACGGCGGTGGAGGCAGCGAAGGCCTACGA
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                                                                                                                                                                                                                                                                                                                                                     Score 80.4; DB 4; Pred. No. 9.1e-14; 0; Mismatches 56
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Pred. No. 1.7e-15;
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Samaha, Raymond Zhang, James Adam, Luc

Application US/09533029

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APPLICANT: Ratcliffe, Oliver
APPLICANT: Pilgrim, Marsha
APPLICANT: Pilgrim, Marsha
APPLICANT: Pilgrim, Marsha
APPLICANT: Reuber, Lynne
TITLE OF INVENTION: DISBASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-010
CURRENT APPLICATION NUMBER: US/09/533,029
CURRENT FILING DATE: 2000-03-22
FEARLIER APPLICATION NUMBER: 60/125,814
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER APPLICATION NUMBER: 50/125,814
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin Ver. 2.1
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US-09-640-211A-1502
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                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1502
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1502
LENGTH: 347
                                                                                                                                                Best
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                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wood, Marion APPLICANT: Shenk, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
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Local Similarity 66.0%;
                                                                                                                                                Local
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376 AAGAAAGGATCCAGGATTTGGTTGGGTACATACGAGACACCTGAGGATGCAGCATTGGCT 435
                                         214 TACAGAGGAGTGAGGAGGCGGCCATGGGGAAAATATGCAGCAGAGATAAGAGACCCCAAG
                                                                                316 TATAAGGGCGTTAGACGGCGGCCGTGGGGGAAGTTCGCGGGGGAGATAAGGGATCCGAAA 375
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                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGAGGAAGAATCAATACCGAGGGATTAGGCAGCGTCCTTGGGGAAAATGGGCTGCGGA
                                                                                                                            Conservative
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                                                                                                                     9.3%; Score 73.8; DB 4; 74.4%; Pred. No. 7.1e-12; tive 0; Mismatches 32;
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Pred. No. 66
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                                                                                                                                                                 Length 347;
                                                                                                                            Indels
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                                                                                                                          Gaps
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GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF EQ ID NOS: 2368
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1293
                                                                              GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Annette
APPLICANT: Glenn, Matthew
ITITLE OF INVENTION: Compositions and Methods for the
ITITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FASTSEQ for Windows Version 4.0
SECTION 1546
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; LENGTH: 390
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-1546
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 1546, Application US/09640211A Patent No. 6833446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity 60.7%;
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TYPE: DNA
ORGANISM: Eucalyptus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387 CAGGATTTGGTTGGGTACATACGAGACACCTGAGGATGCAGCATTGGCTTATGATGCAGC 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 GCGCCGGCGG-CGTGGGGGAAGTTCGCGGCGGAGATACGCGACCCGACGCGCAAGGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 CCCCCGGGCCGAGCCGTCGGGCTCCGCTGGCGGCGACGACGACGACAAGCACTACCGGGGCGT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 CCCGCCAGAAGCGGCCGGCCGGAGGAGGAGGTTCGGAAGGATTGGAACCGGTATAAGGGCCGT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436 TATGA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 AAGAACGGCGCGAGGATTTGGCTCGGGACTTACGAGCTGCCTGAGGACGCGGCATTGGCC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCGTTTAATATGCGTGGAGCTAAAGCTAGGCTTAATTTTCCTC 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCGTTTAGGCTCCGCGGGAGCAAGGCCATCCTGAACTTCCCGC
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Pred. No. 1.4e
0; Mismatches
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1.4e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Modification of Gene Transcription FILE REFERENCE: 11000.1021C1U CURRENT APPLICATION NUMBER: US/09/640,211A CURRENT FILING DATE: 2000-08-16 NUMBER OF SEQ ID NOS: 2368 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 549 LENGTH: 1163
                                                                                                                                                                                                                                                                                                                                    Matches 154;
                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6833446 GENERAL INFORMATION:
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                                                                                                                                                                                                                                298 TCGAAGGATTGGAACCGGTATAAGGGCGTTAGACGGCGGCCGTGGGGGAAGTTCGCGGCG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48
                                                                                                                                                              AGGAAGAGAAAAATGTTTACAGAGGTATCAGACAGCGTCCATGGGGAAAATGGGCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGATGCAGCATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAGG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGAAGAGAAAAAATGTTTACAGAGGTATCAGACAGCGTCCATGGGGAAAATGGGCTGCG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGAAGGATTGGAACCGGTATAAGGGCGTTAGACGGCGGCGCGTGGGGGAAGTTCGCGGCG 357
CTAAATTTTGCTGATAACTCGTGTTCTGTTA 640
                             CTTAATTTTCCTCATTTGATTGGTTCGAATA 508
                                                              GAGGAGGCCGCCAAGGCCTATGATGCAGCGGCTAAAAGGATCCGAGGTAAGAAAGCTAAG
                                                                                              GAGGATGCAGCATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAGG 477
                                                                                                                               GAGATTCGAGATCCCAGTAAG----GGGGTTAGGGTTTGGCTTGGAACGTTCAACACGGCA
                                                                                                                                                                                                                                                                AGAAGTGAGGTGATTCCTCCTTTGGAAGATGTGGAAGGGTCCACACCCACGATTGGGGGG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTAAATTTTGCTGATAACTCGTGTTCTGTTA
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Glenn, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTAATTTTCCTCATTTGATTGGTTCGAATA 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAAGTGAGGTGATTCCTCCTTTGGAAGATGTGGAAGGGTCCACACCCACGATTGGGGGG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shenk, Michael A.
                                                                                                                                                                                                                                                                                                                                    Conservative
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56.8%;
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Pred. No. 3.1e-11;
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RESULT 13

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APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION UNUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1872
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                                                                                                                                                                                                ; LENGTH: 447
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-1872
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                                                                                                                                       Query Match 9.1%;
Best Local Similarity 62.9%;
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Best Local Similarity
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LENGTH: 447
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APPLICANT: Shenk, Micha
APPLICANT: McGrath, An
APPLICANT: Glenn, Mattl
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                                                                              292 GGTTGTTCGAAGGATTGGAACCGGTATAAGGGCGTTAGACGCCGCGGCGCGGGAAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242
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129;
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                                        GGTATTGCAAGGCCTGCCAAGCTCTACAGAGGAGTGAGACAGAGGCACTGGGGGAAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTAGGCTTAATTTTCCTCATTTGA 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAAGGCTTAATTTTCCGGACTTGA 266
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McGrath, Annette
Glenn, Matthew
                                                                                                                        Conservative
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                                                                                                                Score 72.2; DB 4;
Pred. No. 2.4e-11;
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Pred. No. 2.4e-11;
0; Mismatches 73
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Sequence 436, Application US/09640211A

Patent No. 6833446

GENERAL INFORMATION:

APPLICANT: Mood, Marion

APPLICANT: Mood, Marion

APPLICANT: Shenk, Michael A.

APPLICANT: Glenn, Matthew

ITITLE OF INVENTION: Modification of Gene Transcription

FILE REFERENCE: 11000.1021C1U

CURRENT APPLICATION NUMBER: US/09/640,211A

CURRENT APPLICATION NUMBER: US/09/640,211A

CURRENT FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2368

SOFTWARE: FRANCEQ for Windows Version 4.0

LENGTH: 1775

TYPE: DNA

ORGANISM: Pinus radiata
Search completed: March 7, 2005, 19:15:40 Job time: 187 secs
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US-09-640-211A-436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242
                                                                                                                                                                                                                                                                                                                                               573
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                                                                                                                                                                                                                                                                                                                                                                                                                                  513 GTTTCGAGCTTCCTTTAGCTCGGGGTCTTGATGGACCGGCGGCCAAGAGCGCGCGGTGAGAA 572
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                                                                                    750
                                                                                                                                                                     690 AAGCTGCTCGGGCTTATGATGCAGCTGCACGAAAGATCAGAGGTAAGAAGGCGAAAGTAA 749
                                                                                                                                                                                                                                                                                                362 TAAGGGATCCGAAAAAGAAAGGATCCAGGATTTGGTTGGGTACATACGAGACACCTGAGG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACACCTGAGGATGCAGCATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAA 471
                                                                                                                           ATTTTCCTCAT 492
                                                                                                                                                                                                  ATGCAGCATTGGCTTAIGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAGGCTTA 481
                                                                                                                                                                                                                                                        TCAGGGATCCCAGA---AAAGGCGCTAGGGTTTGGCTGGGTACCTTTAATACGGCGGAGG 689
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

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19: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

20: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

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21: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

22: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
                                                                                                                                                                                                                                                            Match Length
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12 US-09-770-149-325

13 US-10-225-068-127

14 US-10-374-780A-5

17 US-10-412-6998-27

18 US-09-777-207-1

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19 US-10-341-961A-193

10 US-10-424-599-30914
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Sequence 299, App
Sequence 2215, Ap
Sequence 2215, App
Sequence 325, App
Sequence 177, Appl
Sequence 5, Appli
Sequence 27, Appli
Sequence 193, Appl
Sequence 193, Appli
Sequence 2984, A
Sequence 30914, A
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102	102	102.4	102.6	103.6	103.6	103.6	103.6	103.6	104.8	106.4	106.4	109.4	110.6	٠	•	110.6	110.6	•	110.6	110.6	•		112.2		٠		113.6		٠	116.2	118.2	118.2
12.9	12.9	12.9	13.0		13.1			13.1	13.2	13.4	13.4	13.8	14.0				•	•		14.0	14.0		14.2				14.3	٠	•	14.7	14.9	14.9
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Sequence 153, App Sequence 101, App	153,	Sequence 232, App	19,		Sequence 9, Appli			17					æ		669,	2073			1475	Sequence 154, App	154, A		979,		478,	32647	999,	498, 1	360	Sequence 4, Appli	e 978	Sequence 477, App

#### ALIGNMENTS

US-10-739-930-299

Sequence 299, Application No. US200 GENERAL INFORMATION:

Application US/10739930 o. US20040216190A1

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                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KOVAlic, David K.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT FPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 299
LENGTH: 940
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                   Query Match 17.1%;
Best Local Similarity 64.2%;
Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
351 CGCCGAGGCAGAAGGGGATGCAGTACAGAGGAGGAGGAGGAGGAGGAGTGAGGAATTCG
                                                                                                                                                   291 CCGTTACCTCTCCGGCGGAGGAAGATAAGCCTCCGGCGACGAAGGCCAAGTGGCTCACACG
                                                                                                                                                                                             233 CGGAAAGCTGTCAGGAGGATTCTGTTGTGGGAACCCCGCCAGAAGCGGCGGCCGGAGGAG
                                                                                                           GTTGTTCGAAGGATTGGAACCGGTATAAGGGCGTTAGACGGCGGCGCCGTGGGGGAAGTTCG
                                                                                                                                                                                                                                   Score 135.6; DB 18; Length Pred. No. 1.8e-25; O; Mismatches 114; Indels
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RESULT 3
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SEQ ID NO 2215
LENGTH: 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2215, Application US/09938842A Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/27,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2001-08-27
PRIOR FILING DATE: 2001-08-28
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                                                                                     CTCGCCGTCGCTCGCCGG
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                                                                                                                                                                        CTAAGCTGAATTTTCCGCATTTGATTGGTTCTTGTAAGTATGAGCCGGTTAGGATTAGGC
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Shu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIF1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-06-22
NUMBER OF 5EQ ID NOS: 5379
SEQ ID NO 2215
CENTRE OF SEQ ID NOS: 5379
SEQ ID NO 2215
PRIOR APPLICATION SECONDARY SECO
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US-09-770-149-325
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 325, Application US/09770149 Patent No. US20020059663A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
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Matthew, Abraham V.
Ledford, Brooke L.
Woesener, Jeffrey P.
Haas, William David
Garcia, Carlos A.
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Rameaka, Joshua G.
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Hamilton, Carol
Price, Jennifer
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Pred. No. 4e-25;
0; Mismatches 1
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APPLICANT

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RESULT 5
US-10-25-068-127
; Sequence 127, Application US/10225068
; Publication No. US20030217383A1
; GENERAL INFORMATION:
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; ORGANISM: Arabidopsis thaliana
US-09-770-149-325
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SEQ ID NO 325
LENGTH: 685
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Best Local Similarity 63.8%;
Matches 203; Conservative
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APPLICANT:
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APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: DATE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
FILE REFERENCE: 514442002040
CURRENT APPLICATION NUMBER: US/10/225,068
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/336,049
                                                                                                                                                                                                                                                                                                 APPLICANT: Mendel Biotechnology, APPLICANT: Reuber, T. Lynne APPLICANT: Riechmann, Jose Luis
                                                                                                     APPLICANT: Broun, Pierre E.
TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND
TITLE OF INVENTION: POLYPEPTIDES IN PLANTS
                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                 Dubell, Arnold T. Ratcliffe, Oliver Pineda, Omaira
                                                                                                                                                                                                                                          Heard, Jacqueline E.
Jiang, Cai-Zhong
Adam, Luc J.
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Allen, Keith
                                                                                                                                                                    Yu, Guo-Liang
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Pred. No. 4.1e-25;
0; Mismatches 115;
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                                                                                                                                                                                                                                                                                                    APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Riechmann, Jose Luis
APPLICANT: Haard, Jacqueline B
APPLICANT: Heard, Jacqueline B
APPLICANT: Haake, Volker
APPLICANT: Creelman, Robert A
APPLICANT: Ratcliffe, Oliver
APPLICANT: Adam, Luc J
APPLICANT: Adam, Luc J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/10374780A Publication No. US20040019927A1
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SEQ ID NO 127
LENGTH: 913
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 203; Conserv
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN
FILE REFERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR PILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR PILING DATE: 2001-08-09
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-11-19
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ORGANISM: Arabidopsis thaliana
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (81)...(761)
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Dubell III, Arnold
Pineda, Omaira
                                                                                                                                                                                                                                              Reuber, T. Lynne
Keddie, James
Broun, Pierre E
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Pred. No. 4
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. 4.7e-25;
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PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,067
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
                                                                                                                                                                                         Sequence 27, Application US/10412699B
Publication No. US20040045049A1
GENERAL INFORMATION:
APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: Fromm, Michael E.
APPLICANT: Heard, Jacqueline E.
APPLICANT: Heard, Jacqueline E.
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 913
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 16.9%;
Local Similarity 63.8%;
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FILING DATE: 2001-12-11
APPLICATION NUMBER: 10/171,468
FILING DATE: 2002-06-14
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FILING DATE: 2001-08-22
APPLICATION NUMBER: 60/336,049
FILING DATE: 2001-11-19
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Samaha, Raymond R.
Pilgrim, Marsha L.
Creelman, Robert A.
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                                                                                   Pineda, Omaira
Reuber, T. Lynne
Keddie, James S.
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Adam, Luc J.
                                                                                                                                           Broun, Pierre E.
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Pred. No. 4.7e-25;
0; Mismatches 115;
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SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 913
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G22
US-10-412-699B-27
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PRIOR APPLICATION NUMBER: 09/394,519
PRIOR APPLICATION NUMBER: 09/489,376
PRIOR APPLICATION NUMBER: 09/489,376
PRIOR APPLICATION NUMBER: 09/506,720
PRIOR FILING DATE: 2000-01-21
PRIOR PRILING DATE: 2000-02-17
PRIOR PRILING DATE: 2000-03-2
PRIOR PRILING DATE: 2000-03-2
PRIOR PRILING DATE: 2000-03-2
PRIOR PRILING DATE: 2000-03-2
PRIOR APPLICATION NUMBER: 09/533,392
PRIOR APPLICATION NUMBER: 09/533,392
PRIOR PILING DATE: 2000-03-2
PRIOR APPLICATION NUMBER: 09/53,648
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2001-03-2
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Best Local
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APPLICANT: Kumimoto, Roderick
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: Polynucleotides and Polypeptides
PILE REFERENCE: MBI-0048CIP
CURRENT APPLICATION NUMBER: US/10/412,699B
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Local 5.
203;
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571
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Similarity 63.8%;
                                                                                           CTAAGCTGAATTTTCCGCATTTGATTGGTTCTTGTAAGTATGAGCCGGTTAGGATTAGGC
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                                            CGAGAAAACGTTTCCCTG
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CTCGCCGTCGCTCGCCGG
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Pred. No. 4.7e-25;
0; Mismatches 115;
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RESULT 8
US-09-777-207-1
(Sequence 1, Application US/09777207
Publication No. US20020039780A1
GENERAL INFORMATION:

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NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 708
TYPE: DNA
ORGANISM: Nicotiana tabacum
US-09-777-207-1
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US-10-341-961A-193
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              CURRENT APPLICATION NUMBER: US/10/341,961A
CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: 60390249
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: 60261029
PRIOR APPLICATION NUMBER: 60261029
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60348792
PRIOR FILING DATE: 2002-01-14
NUMBER OF SEQ ID NOS: 395
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APPLICANT: Martin, Gregory
APPLICANT: Ekengren, Sophia
TITLE OF INVENTION: PLANT DEFENSE-RELATED GENES REGUI
TITLE OF INVENTION: INTERACTIONS AND METHODS OF USE
FILE REFERENCE: BTI.67A2
                                                                                                                                                                                                                                                                                                                     APPLICANT: Boyce Thompson Institute for Plant Research, APPLICANT: Curagen Corporation APPLICANT: Crasta, Oswald
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APPLICANT: Jepson, Ian
TITLE OF INVENTION: New Salicylic Acid Inducible
FILE REFERENCE: PB/5-50067A
CURRENT APPLICATION NUMBER: US/09/777,207
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US60/095,187
PRIOR FILING DATE: 1998-08-03
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTCCTCATTTGATTGGTTCGAATATTTCCGGACCCGTTAGAGTAAACCCGAGAAAACGT 543
                                                                                                                                                                                                                                                                                Swirsky, Peter
Mysore, Kiran
                                                                                                                                                                                                                                                                                                                                                                                                          Application US/10341961A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chua, Nam-Hai
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                                                                                                                                                                                                                                                                                                      Peter
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                                                                                                                                                                                                             REGULATED IN RESPONSE TO PLANT-PATHO
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LENGTH: 437
                                                                                                                                                                                                                                                Matches 153;
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Glycine max FEATURE:
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GCTTAATTTTCCTCATTTGATTGGTTCGAAT 507
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; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-10-341-961A-193
                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: UC-GMROPIC008H09_FLI US-10-425-114-29849
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven B
APPLICANT: Screen, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 29849
LENGTH: 995
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 29849, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
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Local Similarity 69.0%;
les 176; Conservation
                                                                                             450 GGAGATTAGGGACACTAAGAGGAATGGTGTGAGAGTGTGGCTTGGAACCTACGAAACCGC
                                                                                                                                  390 TCCAAAGAAGGGGTTGAGCTACCGAGGCGTGCGGAGGAGGCCGTGGGGGAAGTATGCGGC
                                                                                                                                                                                                                                  297 TTCGAAGGATTGGAACCGGTATAAGGGCGTTAGACGGCGGCCGTGGGGGAAGTTCGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 TATGATAAAGCTGCTTATAGAATGAGAGGATCAAAAGCACATTTGAATTTCCCGCACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 TATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAGGCTTAATTTTCCTCATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 TATAAGGGCGTTAGACGGCGGCCGTGGGGGAAGTTCGCGGCGGAGATAAGGGATCCGAAA 375
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TGAGGATGCAGCTTTAGCTTATGATCGAGCTGCATTTAAGATGCGGGGCTCAAAAGCTAA
                                  TGAGGATGCAGCATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAG
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                                                                                                                                                                                                                                                                                                   14.9%;
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                                                                                                                                                                                                                                                                            Score 118.2; DB Pred. No. 8e-21; O; Mismatches
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Pred. No. 8.8e-24;
0; Mismatches 79;
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RESULT 12
US-10-374-780A-477/c
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US-10-424-599-30914/c
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 477, Application US/10374780A Publication No. US20040019927A1
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SEQ ID NO 30914
LENGTH: 999
                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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Best Local Similarity
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Publication No. US20040031072A1
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                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                    APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cal-Zhong
              TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS FILE REFERENCE: MBI-0047 CIP CURRENT APPLICATION NUMBER: US/10/374,780A CURRENT FILING DATE: 2003-02-25
                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                            APPLICANT:
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APPLICANT: Kovalic David K
                                                                                                                                                                                                                   APPLICANT:
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ORGANISM: Glycine max
FEATURE:
APPLICATION NUMBER: 09/837,944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTTAATTTTCCTCATTTGATTGGTTCGAAT 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAGGATGCAGCTTTAGCTTATGATCGAGCTGCATTTAAGATGCGGGGCTCAAAAGCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGAGGATGCAGCATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAG 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCAAAGAAGGGGTTGAGCTACCGAGGCGTGCGGAGGAGGCCGTGGGGGAAGTATGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCGAAGGATTGGAACCGGTATAAGGGCGTTAGACGGCGGCCGTGGGGGAAGTTCGCGGC 356
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Keddie, James
Broun, Pierre E
                                                                                    Yu, Guo-Liang
                                                                                                     Pilgrim, Marsha L
Dubell III, Arnold T
Pineda, Omaira
                                                                                                                                                                                                                 Adam, Luc J
                                                                                                                                                                                                                                  Creelman, Robert A
Ratcliffe, Oliver
                                                                                                                                                                                                                                                                      Heard, Jacqueline E
Haake, Volker
                                                                                                                                                                                                                                                                                       Heard,
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); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 477
LENGTH: 1049
TYPE: DNA
ORGANISM: Glycine 1
                                                                                                                                                                                                                                                                                                                    Matches 153;
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
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PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,068
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NUMBER OF SEQ ID NOS: 2906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR APPLICATION NUMBER: 60/338,692
R FILING DATE: 2001-12-11
DR APPLICATION NUMBER: 10/171,468
DR FILING DATE: 2002-06-14
DR APPLICATION NUMBER: 10/225,066
DR FILING DATE: 2002-08-09
DR FILING DATE: 2002-08-09
DR FILING DATE: 2002-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-08-09
APPLICATION NUMBER: 09/934,455
FILING DATE: 2001-08-22
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469 GCTGAATTTTCCTCATTTAATTGGCTCGGAT
                                                                                                             417 TGAGGATGCAGCATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAG 476
                                                                                                                                                      589 GGAGATTAGGGACACTAAGAGGAATGGTGTGAGAGTGTGGCTTGGAACCTACGAAACCGC
                                                                                                                                                                                       649 TCCAAAGAAGGGGTTGAGCTACCGAGGCGTGCGGAGGAGGCCGTGGGGGAAGTATGCGGC
                                                                                                                                                                                                                                                                          297 TTCGAAGGATTGGAACCGGTATAAGGGCGTTAGACGGCGGCCGTGGGGGAAGTTCGCGGC
                                                                                                                                                                                                                                                                                                                                    Similarity
                    GCTTAATTTTCCTCATTTGATTGGTTCGAAT 507
                                                                          TGAGGATGCAGCTTTAGCTTATGATCGAGCTGCATTTAAGATGCGGGGCTCAAAAGCTAA
                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 8.2e-21;
0; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                         DB 17;
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RESULT 13 US-10-412-699B-978/c ; Sequence 978, Applica Publication No. US200 ; GENERAL INFORMATION: ; APPLICANT: Mendel Bi APPLICANT: Zhang, M ; APPLICANT: Heard, J APPLICANT:
APPLICANT:
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APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:
APPLICANT: APPLICANT: APPLICANT: T: Ratcliffe, Oliver
T: Kumimoto, Roderick
T: Sherman, Bradley K.
INVENTION: Polymucleotides and Polypeptides in Plants Yu, Guo-Liang Jiang, Cai-Zhong Samaha, Raymond R. Pilgrim, Warsha L. Creelman, Robert A. DuBell, Arnold N. Pineda, Omaira Reuber, T. Lynne Keddie, James S. Riechmann, Jose I Adam, Luc J. Broun, Pierre E. Fromm, Michael E. Heard, Jacqueline E. Application US/10412699B o. US20040045049A1 Biotechnology, Jose Luis

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J Sequence 4, Application US/10122822

Publication No. US20030084477A1

GENERAL INFORMATION:
APPLICANT: Purdue Research Foundation
TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN
FILE REFERENCE: 7024-511
CURRENT APPLICATION NUMBER: US/10/122,822
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 09/202,161
PRIOR APPLICATION NUMBER: US 09/202,161
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: 60/046,494
PRIOR FILING DATE: 1997-05-14
PRIOR APPLICATION NUMBER: 60/046,494
PRIOR FILING DATE: 1997-05-14
PRIOR APPLICATION NUMBER: 60/046,494
PRIOR FILING DATE: 1997-05-14
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-10-122-822-4
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PRIOR APPLICATION NUMBER: 09/394,519
PRIOR FILING DATE: 1990-09-13
PRIOR PELIVATION NUMBER: 09/489,376
PRIOR PELIVATION NUMBER: 09/489,376
PRIOR PELICATION NUMBER: 09/506,720
PRIOR PELICATION NUMBER: 09/506,720
PRIOR APPLICATION NUMBER: 09/533,030
PRIOR APPLICATION NUMBER: 09/533,030
PRIOR PELIVAGE DATE: 2000-03-22
PRIOR PELIVAGE DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
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Matches 153
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SOPTWARE: PatentIn version 3.2
SEQ ID NO 978
LENGTH: 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/713,994
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 09/819,142
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/019,633 PRIOR FILING DATE: 1996-06-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Glycine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/533,029 FILING DATE: 2000-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/533,648 FILING DATE: 2000-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/532,591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-03-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 TTCGAAGGATTGGAACCGGTATAAGGGCGTTAGACGGCGGCCGTGGGGGAAGTTCGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAGGATGCAGCTTTAGCTTATGATCGAGCTGCATTTAAGATGCGGGGCTCAAAAGCTAA
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Pred. No. 8.2e-21;
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US-10-739-930-3666
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; ORGANISM: Lycopersicon esculentum
US-10-122-822-4
                                                                                                                                                                                                                                                                                                                                               US-10-739-930-3666
                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: KOVALIC, DAVID K.
APPLICANT: KOVALIC, DAVID K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 3666
LENGTH: 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3666, Application US/10739930
Publication No. US20040216190A1
                                                                                                                                                                                                                                                                           Matches 146;
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Best Local Similarity
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Best Local Similarity
Matches 177; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Clone ID: GLYMA-23APR03-CLUSTER5319
                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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476
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                                                                                                                                    356
                                                                                                                                                        367 GATCCGAAAAAGGAAAGGATCCAGGATTTGGTTTGGGTACATACGAGACACCCTGAGGATGCA
                                                                                                                                                                                                        296 TGGAAGCGTTACCGGGGCGTGAGGCCTAGACCTTGGGGCAAGTTCGCGGCGGAAATAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312 CGGCAGCTCCGGCGGCTGAAACACCGGAAAAGAAGACATTATAGAGGCGTTTAGACAGCGTC
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                                  CCTCATTTGATTGGTTC 503
                                                                                                  GCATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAGGCTTAATTTT
                                                                                                                                    GATCCAAAGAAGAATGGTGCTAGGATATGGCTTGGGGACTTACGAAACTGAAGAAGAAGCG
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Pred. No. 2.6e-20;
0; Mismatches 83;
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Search

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Job time : 599 secs

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Maximum Match 100%
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Maximum DB seq length: 200000000
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Copyright (c) 1993 - 2005 Compugen Ltd.
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BE449392 EST356151
AV822925 AV822925
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BG587407 EST3489179
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EST541898	USDA-FP_1	R_Eb004	R_Eb014	R_Eb004	EST484022	EST670369	EST486659	EST714097	EST714096	EST596620	QHM9009.y	EST624497	EST624498	UCRPT01_0	EST637769	EST741917	QHM1I18.Y	EST723803	EST724970	20070 000

## ALIGNMENTS

	source	FEATURES					COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	CK715561/c	PECII T 1
/mol_type="mRNA" /cultivar="Hawaii7996" /cultivar="Hawaii7996" /db xref="taxon:4081" /clone="LERSF01B02" /tissue_type="root and collar" /tissue_type="root and collar" /dev_stage="Three weeks old" /lab_host="XL1-Blue" /lab_host="XL1-Blue" /clone_lib="Subtractive cDNA library prepared from tomato /clone_with Ralstonia solanacearum (Rs-Ck)" /note="Vector: pGEM-T EZ; Plant samples were provided by Dr. Jaw-Fen Wang (Tainan, AVRDC). Each plant grown in a 3-inch pot was inoculated with 30 ml (108cfu/ml) of Rs 3-inch pot was inoculated with 30 ml (108cfu/ml) of Rs	/organism="Lycopersicon esculentum"	Location/Qualifiers	01 row: B column: 02	<pre>Email: chiuping@gate.sinica.edu.tw Insert Length: 605</pre>	Fax: 886-2-2561-5600	Nankang, Taipei, 115, Taiwan, Republic of China Tel: 886-2-2652-2268	Crop Plant Improvement Group	Unpublished (2004)	l genomics study of tomato	Lin.W.C. Cheng.M.L. Ting.H.M. and Cheng.C.P.	1 (bases 1 to 605)	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Lycoperatcon esculentum (comaco)	EST.	CK715561.1 GI:50879390		LERSF01B02 Subtractive cDNA library prepared from tomato infected with Ralstonia solanacearum (Rs-Ck) Lycopersicon esculentum cDNA	CK715561 605 bp mRNA linear EST 01-AUG-2004		

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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL COMMENT
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CN385373
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 GATTGGAACCGGTATAAGGGCGTTAGACGGCGGCGGTGGGGGGAAGTTCGCGGCGGAGATA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 GATTGGAACCGGTATAGAGGCGTCAGGCGGCGGCCGTGGGGTAAGTTCGCGGCGAGATA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
spermatoshyta; Magnollophyta; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lycopersicon esculentum CN385373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CN385373 944 bp mRNA linear EST 31-AUG-2004 LE2TR03G24 Tomato CL5915 roots under different developmental stages Lycopersicon esculentum cDNA clone LE2TR03G24, mRNA sequence.
                                                                                                                                                                                                                                                               Email: kyto@gate sinica.edu.tw
Insert Length: 944 Std Error:
Plate: 03 row: G column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kin-Ying, To
Crop Plant Improvement Group
Institute of BioAgricultural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 944)
Wang, C.K., Chen, P.Y., Wang, H.M.,
DNA microarray profiling of gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       devel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCCCTGCGGAGCCTTCTACGACGTCGTCGTCTTCTTCTTC 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTCCTCATTTAATCGGCTCGGACATATCTGAGCCAGTTAGAGTGGCTCCGCGTAAGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGCATTGGCCTTATGACCAAGCCGCTTATAAGATTCGTGGCTCTAAGGCTCGATTGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAGCATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAGGCTTAAT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAGACCCCGATAGGAAAGGTGCTAGGCTTTGGCTAGGGACTTACGGGACACCTGAAGAT
                                                                                                                                                                                                                                                                                                                                                  Academia Rd. Section 2, Taipei, Taiwan 11529 : 886-2-2653-3161
                                                                                                                                                                                                                                     primer: smart2.
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                                                      /db_xref="taxon:4081"
/clone="LE2TR03G24"
                                                                                                             /mol_type="mRNA"
/cultivar="CL5915"
                                                                                                                                                            organism="Lycopersicon"
                                                                                                                                                                                                           Location/Qualifiers
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Pred. No. 1.8e-31;
0; Mismatches 75
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CN385772 673 bp mRNA linear EST 31-AUG-2004 LE2TR04I02 Tomato CL5915 roots under different developmental stages Lycopersicon esculentum cDNA clone LE2TR04I02, mRNA sequence.
                                                                                                                                                                       Email: kyto@gate.sinica.edu.tw
Insert Length: 673 Std Error:
Plate: 04 row: I column: 02
                                                                                                                                                                                                                                                       Crop Plant Improvement Group
Institute of BioAgricultural Science
128 Academia Rd. Section 2, Taipei,
Tel: 886-2-2653-3161
                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 673)
Wang, C.K., Chen, P.Y., Wang, H.M.,
DNA microarray profiling of gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                                                                                                                            Contact: Kin-Ying,
                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                         development
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                                        /mol_type="mRNA"
/cultivar="CL5915"
                                                                                                                          Location/Qualifiers
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/lab_host="B.coli BM25.8"
                                                                                organism="Lycopersicon"
clone="LE2TR04I02"
                      db_xref="taxon:4081"
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70.0%;
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Pred. No. 9.9e-30;
0; Mismatches 89
                                                                                                                                                                                                                                                                                Sciences, Academia Sinica
Faipei, Taiwan 11529
                                                                                                                                                                                                                                                                                                                                                                                                           Soong, S.C., Chen, S.C. and To, expression during tomato root
                                                                                    esculentum"
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CK936905

CK936905

CGF1004516 G04 Developing fruit flavedo at 80 DAFB Citrus sinensis cDNA clone F80DAB0002_IIIF_G04 5', mRNA sequence.

CK936905

CK936905.1 GI:45450103

EST.

Citrus sinensis

Citrus sinensis

Citrus sinensis

Citrus sinensis

Eitrus sinensis

Eitrus sinensis

Eitrus sinensis

Eitrus sinensis

Eitrus sinensis

Eitrus sinensis

Formatophyta; Wagnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Rutaceae; Citrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Abhaya Dandekar, PhD
CAES Genome Facility
UC Davis, Department of Pomology
One Shields Ave, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 530 752 7784
Fax: 530 752 8502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Analysis of peel specific 
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Uratsu,S., Baek,J., Leslie,A., Xu,J., Cook,D. and Dandekar,A
Analysis of peel specific genes in Citrus (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAAGCCTTAATTTTTCCTCATTTG 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              il: amdandekar@ucdavis.edu
primer: WSC-F-TCCGAGATCTGGACGAGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                 /organism="Citrus sinensis"
/mol_type="mRNA"
/cultivar="Washington navel orange"
/db xref="taxon:2711"
/clone="r80DAB0002_IIIF_G04"
/sex="Hermaphrodite"
/cell_type="Fallvedo"
/dev_stage="Developing fruit sample-color_stage="Developing fruit sample-color_stage="Developing">Developing fruit sample-color_stage="Developing fruit sample-color_stag
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developmental stages"
/dev_stage="Developing fruit sample-collected July 2003"
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/lab_host="E.coli BM25.8"
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. No. 2.5e-29;
ismatches 90;
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Best Local Similarity 67.8%;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 903)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:

A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNSOA88X

903 bp mRNA linear HTC 06-FEB-20
Arabidopsis thaliana Full-length cDNA Complete sequence from clou
GSLTSIL77ZE09 of Silique of strain col-0 of Arabidopsis thaliana
                                                                                                                                                                                                                                                                             Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (thale cress).
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/clone="Organ: Fruit; Vector: pTriplEx2; Site 1: SfiIA;
/note="Organ: Fruit; Vector: pTriplEx2; Site 1: SfiIA;
/note="Organ: Fruit; Vector: pTriplEx2; Site 1: SfiIA;
Site 2: SfiIB; Developing citrus fruits were harvested
from trees growing in the 'Citrus variety collection' in
the Wolfskill experimental orchard located in Winters,
California (USA). Fruit was collected on July 29, 2003,
between 8 to 9 am and stored at 4C. The flavedo tissue was
dissected out of developing fruit (80 DAFB) and used to
isolate RNA using Trizol reagent from Invitrogen. The cDNA
Library was constructed using the SMART CDNA library Kit
(Clontech). The primary library was en masse evicted and
plasmid DNA containing the cDNA library was isolated from
the resultant bacterial population. Plasmid DNA was then
transformed into ultra competent E coll cells (XL10 Gold;
Stratagene). Transformants were plated out on Q-trays
(2000 cfu/tray), picked using a Qbot and archived in 384
well dishes."
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Pred. No. 3.6e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - Web: www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V. Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
                                                                                                                                                      AV552445

AV552445 Arabidopsis thaliana roots Co
cDNA clone RZ29h02R 5', mRNA sequence.
AV552445
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                            Arabidopsis thaliana (thale cress) Arabidopsis thaliana
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(bases 1 to 563)
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/clone="GSLTSIL77ZE09"
/tissue_type="Gilique"
/plasmid="pCMVSPORT_6"
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                van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang, F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
                                                                                                                                                                                                                                                     EST356151 L. hirsutum trichome, Cornell University Cornell University Cornell University CONA clone cLHT31K6, mRNA sequence.
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Email: asamizu@kazusa.or.jp, URL:http://www.l
Location/Qualifiers
                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamidds; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 591)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Erika Asamizu
The First Laboratory for Plant Gene
Kazusa DNA Research Institute
                                                                                                                                                                        Lycopersicon hirsutum (Solanum hirsutum)
Lycopersicon hirsutum
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  Generation of ESTs from wild tomato (Lycopersicon hirsutum)
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/clone_lib="Arabidopsis thaliana roots Columbia"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RZ29h02R"
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/ecotype="Columbia"
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65.1%;
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Pred. No. 4.6e-24;
0; Mismatches 105
                                                                                                                                                                                                                                                                                                             591 bp
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Gaps

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379 352

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AUTHORS
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KEYWORDS
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                                                                                                   Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                AV822925 RAFL5 Arabidopsis th
                                        Large scale analysis of Arabidopsis full-length cDNA Unpublished (2002) Contact: Motoaki Seki
                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 663)
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EST.
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                                                                                                                                                                                                                  Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                            and Shinozaki, K.
                                                                                                                                                                                                                                                                                               mRNA sequence.
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Contact: CUGI
Contact: CUGI
Clemson University Genomics Institute
Clemson University
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ilarity 65.9%;
Conservative
             Genomic Sciences Center
                             Functional Genomics Research Group
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/dev_stage="mixed stages"
/clone_lib="L. hirsutum trichome, Cornell University"
/clone_lib="L. hirsutum trichome, Cornell University"
/note="Leaves of various stages were shaken in liquid
nitrogen, shearing off trichomes. This procedure yielded
mixture of cells which is highly enriched for trichome
likely with minor contaminations of other types of leaf
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/clone="cLHT31K6"
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Pred. No. 4.6e-24;
0; Mismatches 100
Ibaraki 305-0074,
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Best Local 9
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                                            Unpublished (2001)
Contact: Doil Choi
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                                                                                                                                                                                                                                  Capsicum annuum
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Capsicum.

1 (bases 1 to 490)

Lee,S., Kim,S.-Y., Chung,Y.-H., Shin,H.-J., Goh,S.-H., Pai,H Hur,C.-G. and Choi,D.

Generation of Expressed Sequence Tags from Hot Pepper (Capsiannuum L.) and Sequence Analysis in Relation to Hypersensitic Response Against Pathogen
Genome Research Center and National Center for Genome Inf
Korea Research Institute of Bioscience and Biotechnology
P.O. Box 115, Yusong, Taejeon, 305-600, Republic of Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                              CA520877
KS11018B10 KS11 Capsicum
CA520877
CA520877.1 GI:25034902
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Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a SstI/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTAGGCTTAATTTTCCTCATTTGATTGGTTCGAATATTTCCGGACCCGTTAGAGTAAAACC
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/note="Site 1: SstI; Site 2:
dehydration-treated(1,2,5,10
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/lab_host="SOLR"
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/db_xref="taxon:3702"
/clone="RAFL05-13-E10"
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Pred. No. 4.8e-24;
0; Mismatches 105
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                                                                                                                                                          Tags from Hot Pepper (Capsicum in Relation to Hypersensitive
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Best Local Similarity
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                                                                                                                                                                                                                                                                1 (bases 1 to 636)
Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S.,
O'Shaughnesey,A.L., Bailja,V., Martienssen,R.A., M
Benfey,P. and Stevenson,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CB078370 636 bp mRNA linear EST 24-JAN-:
hj66g10.g1 Hedyotis terminalis flower - Stage 2 (NYBG) Hedyotis
terminalis cDNA clone hj66g10, mRNA sequence.
                                                                                                                         Tel: 516 367 8884
Fax: 516 367 8874
                                                                                                                                                      Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                     Unpublished (2003)
Contact: W. Richard McCombie
                                                                                                                                                                                                                                     Expressed tag sequences from (NYBG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 82-42-860-4340

Tex: 82-42-860-4309

Fax: 82-42-860-4309

Email: doil@mail.kribb.re.kr

Plate: 018 row: B column: :
                                                                           Plate: hj66 row: g colu
Seq primer: -21M13UnivRev
                                                                                                          Email: mccombie@cshl.org
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Gentianales; Rubiaceae; Rubioideae;
                                                                                                                                                                                                                                                                                                                                                                                         Hedyotis terminalis
                                                                                                                                                                                                                                                                                                                               Spermacoceae; Hedyotis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CB078370.1 GI:27891807
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                                              quality sequence stop: 636.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:4072"
/clone_lib="KS11"
/organism="Hedyotis terminalis"
/mol_type="mRNA"
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Pred. No. 5.1e-24;
0; Mismatches 92;
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AUTHORS
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ORGANISM
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BF275652
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VERSION
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521 TTCCACATATGATTGGATC 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Gossypium arboreum
Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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BF275662
                                                Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
                                                                                                   Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                  Contact: Wing RA
                                                                                                                                                                                                                                                                                   An integrated analysis of the genetics, development, and of the cotton fiber
                                                                                                                                                                                                                                                                                                                                      Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
                                                                                                                                                                                                                                                                                                                                                            Wing, R.A.,
                                                                                                                                                       Clemson University
100 Jordan Hall, Clemson,
                                                                                                                                                                                                          Clemson University Genomics Institute
                                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                     rosids; eurosids II; Malvales; Malvaceae; Malvoideae;
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Similarity 69.5%;
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quality sequence start: quality sequence stop:
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/dev gtage="pre-anthesis; Stage 2"
/dev gtage="pre-anthesis; Stage 2"
/clone lib="Hedyotis terminalis flower - Stage 2 (NYBG)"
/note="Organ: flower; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
CSHI_12/21/01 Library: Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts. Sample: collected on the island of
Hawaii, Hawaii; NYBG herbarium voucher TM2562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:11206722
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/cultivar="8400" /db_xref="taxon:29729" /clone="GA__Eb0024J23f"

/mol_type="mRNA" /strain="AKA"

arboreum"

Location/Qualifiers 1. .903 /organism="Gossypium

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REFERENCE
AUTHORS
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BG128566
LOCUS
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ORGANISM
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Best Local S
Matches 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 TATAAGGGCGTTAGACGGCGGCCGTGGGGGAAGTTCGCGGCGGAGATAAGGGATCCGAAA 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,
Hansen,C., Ronning,C. and Tanksley,S.
Generation of ESTs from tomato shoot/meristem tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
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Lycopersicon esculentum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 652)
                                                                                                                                                                                                                                                                                                                                                                                    Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                    /Glone lib="tomato shoot/meristem"
/note="Vector: pBluescript SK(-); Site 1: EcoR1; Site 2:
Xho1; Small expanding leaves from the growing tip were
taken from greenhouse plants (4-6wks old TA496). Tissue
was immediately frozen in liquid nitrogen."
                                                                                                                                                            /tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                             organism="Lycopersicon esculentum"
|mol_type="mRNA"
|cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Gossypium arboreum 7-10 dpa
/note="Vector: pBK-CMV; Site_1: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="Fibers isolated from
                                                                                                                                                                                                                   clone="cTOF21K4"
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  16.4%;
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Pred. No. 2.8e-23
0; Mismatches 9
  Score 129.8;
  DΒ
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; Site_2:
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 Query Match
Best Local Similarity
Matches 176; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 TTGGAACGTACGAAACAGCTGAAGAAGCTGCAATTGCTTATGATAAAGCTGCTTATAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 CGGCAGCTCCGGCGGCTGAAACACCGAAAGGAAGACATTATAGAGGCGTTAGACAGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato carpel tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 437)
                                                                                                                                                                                                                                                                                                                                                                                                  100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI771213
EST252409 tomato ovary,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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   Conservative
                                                                                                                                                                                                                                                                                                                                                                                      sequence.
                                                                                                      /tissue_type="carpel"
/dev_gtage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XI1-Blue MRF'"
/clone lib="tomato ovary, TAMU"
/note="Vector: pBlueScript SK(-); Site 1: EcoR1; Site 2:
Xho1; CLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector Lamda ZAP II with 5'
and 3' ends located at the EcoRI and XhoI sites,
                                                                                                                                                                                                                                                       /db_xref="taxon:4081"
/clone="cLED29K9"
                                                                                                                                                                                                                                                                                           organism="Lycopersicon/mol_type="mRNA"/cultivar="TA496"
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 Score 128.6; DB 1;
Pred. No. 6.4e-23;
0; Mismatches 79;
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                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
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                                                                              190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 575)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., I
Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
Giovannoni,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lycopersicon esculentum (tomato)
Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW034216 575 bp mRNA EST277787 tomato callus, TAMU Lycopersicon CLEC32P18 similar to Pti4, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW034216.1 GI:5892972
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University Genomics Institute Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: CUGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generation of ESTs from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 Jordan Hall, Clemson,
CGGCAGCTCCGGCGGCTGAAACACCGAAAGGAAGACATTATAGAGGCGTTAGACAGCGTC
                                   CGGCGGCCGGAGGAGGTTGTTCGAAGGATTGGAACCGGTATAAGGGCCGTTAGACGGCGGC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGGCAAGCTCGTCG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCGGTTTGAATGAACCGGAACCGGTTCGAGTTACGGCGAAAAGGCGAGCATCGCCGGAA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTGGTTCGAATATTTCCGGACCCGTTAGAGTAAACCCGAGAAAACGTTTCCCTGCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAGGCTTAATTTTCCTCATTTG 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGAAAGGATCCAGGATTTGGTTGGGTACATACGAGACACCTGAGGATGCAGCATTGGCT 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATAGAGGCGTTAGACAGCGTCCGTGGGGGAAATTTGCGGCGGAGATTAGAGATCCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTTCTACGACGTCG 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGAACGGAGCTAGGGTTTGGCTTGGAACGTACGAAACAGCTGAAGAAGCTGCAATTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="callus"
/dev stage="25-40 days old"
/lab_host="XL1-Blue MRF'"
/clone_lib="comato_callus, TAMU"
/clone_lib="comato_callus, TAMU"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/kno1; supplier: Giovannoni laboratory; cLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed_callus was harvested at 25 and 40 days and included
                                                                                                                                                                             undifferentiated masses. Tomato
                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4081"
/clone="cLEC32P18"
                                                                                                                                                                                                                                                                                                                                                                                                                       cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Lycopersicon
                                                                                               16.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         _type="mRNA
                                                                          Score 128.2; DB 2;
Pred. No. 8.6e-23;
0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tomato callus tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SC 29634,
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                                                                                                                                                                             Callus EST Library"
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VERSION
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medicago truncatula/Glomus versiforme mixed Medicago truncatula/Glomus versiforme mixed EURaryota; mixed EST libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N210846e MHAM Medicago truncatula/Glomus versiforme
library cDNA clone MHAM-7M11, mRNA sequence.
AW584731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other name: MHAM-7a-G06; Date: 3/14/00; Updated to the Database Expressed Sequence Tags (dbEST) on 04/27/00; More information is available at 'http://chrysie.tamu.edu/medicago'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harrison, M.J., Liu, J., Peng, H., Gonzales, M., Ellis, L., Town, C., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C., ESTs from roots of Medicago truncatula after colonization with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant Biology Division
The Samuel Roberts Noble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mjharrison@noble.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Harrison M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glomus versiforme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW584731.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGGTACATACGAGACACCTGAGGATGCAGCATTGGCTTATGATGCAGCCGCGTTTAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sam Noble Parkway,
           /clone lib="MHAAM"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                  /tissue_type="roots colonized with Glomus versiforme" /dev stage="Roots harvested at 10, 17, 22, 31 and 39 post-inoculation with Glomus versiforme. The library made from a mixture of RNA from each of these stages.
                                                                                                                                                                                                                                                                                                                                                          /culTivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
                                                                                                                                                                                                                                   /lab_host="E. coli strain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           /clone="MHAM-7M11"
                                                                                                                                                                                                                                                                                                                                                                                                                               .ibrary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Medicago truncatula/Glomus versiforme mixed
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                                                                                                                                                                                                                                                                                                                                                                                                      _type="mRNA"
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Query Match Best Local Sim Matches 164;

Similarity

16.2%; 73.2%;

Score 128; DB 2; Pred. No. 9.9e-23; 0; Mismatches 60

Length 638

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Gaps

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Conservative

	416 CCCCACCTCATTGGCTCTGATGTGTTTACACCAGAGCCAGAGAA 459	Db 4
	487 CCTCATTTGATTGGTTCGAATATTTCCGGACCCGTTAGAGTAAA 530	Qy 4
CTTAATTTT 41	356 GCTTTGGCTTACGACAAAGCTGCTTTTAAGATGCGTGGCCGAAAGGCCAAGCTTAATTTT 415	Db 3
CTTAATTTT 48	427 GCATTGGCTTATGATGCAGCCGCGTTTAATATGCGTGGAGCTAAAGCTAGGCTTAATTTT 486	Qy 4
GAGGAAGCA 35	296 GATCCAAAAAAGAATGGTGCTAGGGTTTGGCTTGGTACTTATGTGACGGAGGAAGCA 355	Db 2
GAGGATGCA 42	367 GATCCGAAAAAGAAGGATCCAGGATTTGGTTGGGTACATACGAGACACCTGAGGATGCA 426	<b>Q</b> y
GAGATAAGA 29	236 TGGAAGCGGTACAAGGGCGTGAGGCCATGGGGGAAGTTCGCGGCAGAGATAAGA 295	Db 2
GAGATAAGG 36	307 IGGAACCGGTATAAGGGCGTTAGACGGCGGCCGTGGGGGGAAGTTCGCGGCGGAGATAAGG 366	Qy :

Search completed: March 7, 2005, 19:12:35 Job time: 3392 secs

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Minimum DB
Maximum DB
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                                                                                                                                         Database
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geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
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                                                                                     geneseqp1990s:*
geneseqp2000s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

ADM71807 ADM71807 ADM71807 AAX91727 AAX91727 AAX91727 AAX91727 AAB25826 ADM713274 AAB25826 ADM713274 AAB25826 ADM713274 AAM7143274 AMM71807 AMM7180
Add30138 Plant yie

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
16	16	16	16	16	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17
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Aag50951	Aag50952	Aag09634	Ado63660	Adi43273	Ado02947	Adi42694	Adi42040	Ado61543	Ado01641	Add55696	Aae02554	Ado62889	Ado03313	Ado01637	Adi43767	Add30756	Aae02540	Ado62997	Ado61811
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### ALIGNMENTS

# AAY97228 standard; protein; 203 A

Plant transcription factor AP2 DNA-binding domain polypeptide 19-DEC-2000 (first entry) AAY97228;

AP2; transcription factor; plant metabolism; metabolite; primary; secondary; alkaloid; terpenoid indole alkaloid; TIA; pharmaceutical; food colouring; flavouring; fragrance; antimicrobial; pathogenic; insecticide; gene expression; modulation.

Catharanthus roseus.

WO200046383-A2

10-AUG-2000.

07-FEB-2000; 2000WO-NL000075.

05-FEB-1999; 10-FEB-1999; 99DK-00000158. 99US-0119388P.

(UYLE-) RIJKSUNIV LEIDEN.

Memelink J, Van Der Fits CTE, Menke FLH, Kijne JW;

WPI; 200 N-PSDB; 2000-499380/44. DB; AAA53745.

Modulating level of metabolites and stress resistance in recombinant cells for synthesis of plant metabolites such as alkaloids including terpenoid indole alkaloids, by providing transcription factor to the cell.

Disclosure; Page 97-98; 101pp; English.

Many plant secondary metabolites have value as pharmaceuticals, food colourings, flavours and fragrances. Some plant secondary metabolites are linked to plant or plant cell defence mechanisms and may confer to the plant antimicrobial activity, protection against UV light, herbivores, pathogens, insects and nematodes. Plant secondary metabolites such as terpenoid indole alkaloids (TIA) represent a class of pharmaceutically useful compounds which naturally occur in many plant species. New methods are described which modulate the expression of one or more genes involved

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                                                                    The invention relates to pathogen-responsive genes that encode a nematode regulated polypeptides. The proteins of the invention include calcium dependent protein kinase (CDPK), nematode-responsive transcription factor 1 (NRTF1), nematode-responsive protein (NRP), caffeic acid 7-0-methyltransferase (70M) or inositol 5-phosphatase (IPP) polypeptides. The nucleic acid molecule encoding the polypeptides are operably linked to a promoter that drives expression in a host cell. The composition and methods are useful for conferring or improving nematode resistance in
                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic proteins, useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant; nematode-regulated polypeptide; calcium dependent protein kinase; CDPK; nematode-responsive transcription factor 1; NRTF1; nematode-responsive protein; NRP; caffeic acid 7-0-methyltransferase; 70M; inositol 5-phosphatase; IPP; nematocidal; gene therapy; nematode resistance; soybean; enzyme; NRTF1c.
                                                                                                                                                                                                                                                                                                           Claim 26; SEQ ID NO 11; 143pp; English.
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  Sequence 202 AA,
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DB; ADM72372.
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                                                   sequence represents a soybean NRTF1c polypeptide
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                                                                                                                           The invention relates to pathogen-responsive genes that encode a nematode regulated polypeptides. The propoteins of the invention include calcium dependent protein kinase (CDPK), nematode-responsive transcription factor 1 (NRTF1), nematode-responsive protein (NRP), caffeic acid 7-0-methyltransferase (70M) or inositol 5-phosphatase (IPP) polypeptides. The nucleic acid molecule encoding the polypeptides are operably linked to a promoter that drives expression in a host cell. The composition and methods are useful for conferring or improving nematode resistance in plants. The present sequence represents a soybean NRTF1d polypeptide.
                                                                                                                                                                                                                                                                                                    New isolated nucleic proteins, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant; nematode-regulated polypeptide; calcium dependent protein kinase; CDPK; nematode-responsive transcription factor 1; NRTF1; nematode-responsive protein; NRP; caffeic acid 7-O-methyltransferase; 70M; inositol 5-phosphatase; IPP; nematocidal; gene therapy;
                                                                                                   Sequence 202
                                                                                                                                                                                                                                                                Claim 26; SEQ ID NO 13; 143pp; English
                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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)B; ADM72374.
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RESULT 6 AAG24800 ID AAG2

AAG24800 standard; protein; 212

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AC AAG34781;
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              Arabidopsis thaliana protein
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                                                  Protein identification; signal hybridisation assay; genetic matermination sequence.
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                         Arabidopsis thaliana.
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05-MAR-1999;
                                                        25-FEB-2000; 2000EP-00301439
                                                                                           06-SEP-2000
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28-0CT-1999
28-0CT-1999
28-0CT-1999
                                        17-NOV-1999;
17-APR-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                     Transcription factor; environmental plant structure; plant development.
                                                                                                                                                                                                                                           Arabidopsis
                                                                                                14-NOV-2000; 2000WO-US031458
                                                                                                                             25-MAY-2001.
                                                                                                                                                        WO200136598-A1.
                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana transcription factor G22.
                                                                                                                                                                                                                                                                                                                                              10-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match
Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 GVRRRPWGKFAAEIRDPKK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 GVRRRPWGKFAAEIRDPKK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 9.4%;
1 Similarity 100.0%
19; Conservative
 MENDEL BIOTECHNOLOGY INC PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                         ; 99US-0166228P.
; 2000US-0197899P.
; 2000US-0227439P.
                                                                                                                                                                                                                                           thaliana.
                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
89. .157
                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                     protein;
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3-0158232P.
3-0158232P.
3-0159294P.
3-0159295P.
3-0159331P.
3-0159331P.
3-0159331P.
3-0159637P.
3-016968P.
3-0160747P.
3-0160774P.
3-01607
                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                     "Conserved domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J.0%;
0;
                                                                                                                                                                                                                                                                                                                                                                                                        226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19; DB; Pred. No. 3e-0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Ä
                                                                                                                                                                                                                                                                                     stress tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                     gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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99US-0144005P 99US-0144086P 99US-0144331P 99US-0144333P 99US-0144333P 99US-0144333P 99US-0144332P 99US-0144332P 99US-0144632P 99US-0145086P 99US-0145086P 99US-0145085P 99US-0145145P 99US-0145145P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0146388P 99US-0147303P 99US-0147303P 99US-0147303P 99US-0147303P 99US-014973P 99US-014973P 99US-014973P 99US-014973P 99US-0151065P 99US-0151303P 99US-0151303P 99US-0151303P 99US-015375P 99US-0154739P 99US-0154739P 99US-0154739P 99US-0154739P 99US-0154739P 99US-0154739P 99US-0154739P 99US-0155459P 99US-0155459P 99US-0155659P 99US-0155659P 99US-0155717P 99US-015717P 99US-0157117P 99US-0157117P

19-JUL-1999
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23-JUL-1999
24-AUG-1999
27-JUL-1999
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28-JUL-190
28-JUL-

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RESULT 11
ADE37189
ID ADE37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phenotype in desirable ways, such as modifying a plants environmental stress. The transcription factor is encoded by environmental stress tolerance gene derived from Arabidopsis thaliana. The transcription factors and the genes encoding them are used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, onion, cucumber, eggplant, grapes, honey dew, calleflower, mango, melon, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas. These sequences are also used for modifying traits associated with environmental stress tolerance, such as freezing, chilling, heat, drought, water saturation, salt, photoconditions, radiation and ozone. The transcription factors are used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pineda
Reuber
                                                                                                                                                    microbial disease; fungal disease; viral disease; pest infestation; herbicide sensitivity; heavy metal tolerance; heavy metal uptake; growth improvement; photocondition; nutrient uptake; hormone sensit
                                                                                                            Arabidopsis thaliana
                                                                                                                                                                                               transcription factor; tolerance; environmental condition;
                                                                                                                                                                                                                         Plant
                                                                                                                                                                                                                                                                                                          ADE37189 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present amino acid sequence is Arabidopsis thaliana transcription factor. This novel transcription factor is useful for modifying a plant's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding plant transcription factor polypeptides, useful for altering the environmental stress tolerance characteristics of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (YUGG/)
(CREE/)
(RIEC/)
(HEAR/)
(RATC/)
(REUB/)
09-AUG-2001; 2001US-0310847P
                          09-AUG-2002; 2002WO-US026966.
                                                       20-FEB-2003
                                                                                  WO2003014327-A2
                                                                                                                                        transgenic
                                                                                                                                                                                                                                                      29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-336000/35.
                                                                                                                                                                                                                                                                                                                                                                                                  102 GVRRRPWGKFAAEIRDPKK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Page 55-56; 116pp; English
                                                                                                                                                                                                                           yield related
                                                                                                                                                                                                                                                                                                                                                                                  94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YU G.
CREELMAN R.
RIECHMANN J L.
HEARD J.
RATCLIFFE O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REUBER
KEDDIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                  GVRRRPWGKFAABIRDPKK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yu G,
Keddie
                                                                                                                                        plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,
                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 5
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                                                                                                                                                                                                                         protein from
                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'n
                                                                                                                                                                                                                                                                                                            226
                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Riechmann JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                           clone
                                                                                                                                                                                                                           G22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                     sensitivity;
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                                                                                                                                                                                                                                                                                   RESERVATION OF THE STREET CONTRACTOR OF THE ST
                                                                                                                                                                                              Query Match
                                                                                                                                           Matches
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Ratcliffe
                                                                                                                                                                                                                                                                                                                                                                           to environmental conditions, improved tolerance to microbial, fungal or viral diseases, improved tolerance to pest infestation, decreased herbicide sensitivity, improved tolerance of heavy metals, or enhanced ability to take up heavy metals, improved growth under poor photoconditions, improved nutrient uptake, or reduced hormone sensitivity. The transgenic plants are useful for growing a progeny plant comprising the desired trait. The polynucleotides and polypeptides are also useful in bioinformatic search methods. This sequence represents one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-NOV-2001; 2001US-0336049P
11-DEC-2001; 2001US-0338692P
14-JUN-2002; 2002US-00171468
                                                                                                                                                                                                                                                                                   Sequence 226 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins. The isolated or recombinant polynucleotide is useful producing a modified plant with a modified trait, e.g. enhances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a number of cDNA sequence and their encoded proteins which are especially transcription factor cDNAs and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New stress-related transcription factor polynucleotides and polypeptides, useful for producing transgenic plants with e.g. improved tolerance to diseases or pests, decreased herbicide sensitivity, or improved nutrient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MEND-) MENDEL BIOTECHNOLOGY INC
                                                                                                                                                                            Local
                                            102 GVRRRPWGKFAAEIRDPKK 120
94
                                                                                                                                                                                                                                                                                                                                                     proteins
                                                                                                                                           19;
                                                                                                                                                                            Similarity
GVRRRPWGKFAAEIRDPKK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ó
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, Pineda (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                         of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NO 128; 470pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yu ,
                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                         invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heard
Mu GL,
                                                                                                                                           0
                                                                                                                                                                            Score 19;
Pred. No.
                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JE, Jiang
Broun PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English
                                                                                                                                                                            DB 7;
3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ú
                                                                                                                                               0
                                                                                                                                                                                                             Length 226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g. enhanced tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dubell AN;
                                                                                                                                               0
                                                                                                                                               Gaps
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RESULT 12
ADI41543
                                                                          glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; flowering; flower structure; stem bifurcation; branching pattern; apical dominance; trichome; stem morphology; root growth; root hair; seed development; cell proliferation; cell differentiation; premature senescence; necrosis; plant size; leaf morphology; seed morphology; seed biochemistry; root anthocyanin; plant anthocyanin; light response; shade avoidance; bioinformatic;
                                                                                                                                                                                                                                                                                             transgenic; plant; enhanced tolerance to abiotic stress;
                                                                                                                                                                                                                                                                                                                                                           Plant transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADI41543 standard;
Arabidopsis thaliana
                                                          transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                         22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI41543
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                 factor
                                                                                                                                                                                                                                                                                                                                                              #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226
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18-APR-2001; 2001US-00837944 25-FEB-2003; 2003US-00374780 29-JAN-2004

limitation;

germination;

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RESULT 13
ADO01615
ID ADO01
XX
AC ADO01
XX
DT 01-JU
DT 01-JU
XX
Thale
XX
Thale
                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                            Ś
                                                                                                                                                                                                                                                                                                      invention can be used to produced a plant having altered traits such as:
cenhanced tolerance to abiotic stress; glyphosphate tolerance; hormone
sensitivity; disease resistance; sugar sensing; early or late flowering;
altered flower structure, change in stem bifurcations, altered branching
trichomes; reduced apical dominance, reduced trichome density; lack of
trichomes; reduced ectopic trichome number; altered trichome
development; increase in trichome number; altered seed development;
altered cell proliferation or cell differentiation; rapid development;
premature senescence; increased neorosis; increase in seedling or plant
size; decreased plant size; leaf morphology; seed morphology; seed
biochemistry; increase in root anthocyanins; increase in plant
transgenic plant, polynucleotides and polypeptides are useful in
bioinformatic search methods. This is the amino acid sequence of a plant
transcription factor that can be used in the creation of a transgenic
                                                                                                                                                                                                                    Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sherman B
Creelman
                                                                                                                                                                                                                                                                       Sequence
       Thalecress;
                                Thalecress
                                                         01-JUL-2004
                                                                                  AD001615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New transgenic plant comprison more than 500 nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HAAK/)
(CREE/)
(RATC/)
(ADAM/)
(REUB/)
(KEDD/)
(BROU/)
(BROU/)
(DUBE/)
                                                                                                      ADO01615 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pilgrim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHER/)
(RIEC/)
(JIAN/)
(HEAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PINE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention describes a transgenic plant comprising a recombinant ynucleotide of any one of more than 500 nucleotide sequences ful ined in the specification or its complement. The method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2004-132245/13.
DB; ADI41542.
                                                                                                                                                                                             102
                                                                                                                                                                    94
                                                                                                                                                                                                                                                                                               with altered traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CREELMAN R A.
RATCLIFFE O.
ADAM L J.
REUBER T L.
KEDDIE J.
BROUN P E.
PILGRIM M L.
DUBELL A N.
PINEDA O.
YU G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHERMAN B K.
RIECHMANN J L.
JIANG C.
HEARD J B.
                                                                                                                                                                                                                     . Similarity 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ĭ,
                                                                                                                                                                                                                                                                       226
                                                                                                                                                                                     GVRRRPWGKFAAEIRDPKK 120
                                                                                                                                                                    GVRRRPWGKFAAEIRDPKK 112
                               transcription factor protein #14.
transcription factor; plant; transgenic; abiotic stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Riechmann JL,
, Ratcliffe O,
Dubell AN, Pi
                                                                                                                                                                                                                    9.4%; S.larity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                       A,
                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; 435pp; English
                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprising a recombinant leotide sequences, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pineda O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jiang C,
Adam LJ,
                                                                                                        226
                                                                                                                                                                                                                               Score 19;
Pred. No.
                                                                                                        ₽
                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heard JE,
Reuber TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ģ
                                                                                                                                                                                                                               DB 8;
3e-09;
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                                                                                                                                                                                                                                           Length 226;
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Keddie
                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fully
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22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
06-APR-2000;
16-NOV-2000;
27-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2002;
14-JUN-2002;
09-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-1999;
21-JAN-2000;
17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cold tolerance; heat tolerance; drought; osmotic stress; phosphate limitation; potassium limitation; nitrogen limitat. hormone sensitivity; disease resistance; sugar sensing; seed flowering; inflorescence architectural change; meristem cell differentiation; phyllotaxy; apical dominance; trichome development; seed development; premature senescence delayed senescence; lethality; necrosis; plant size; leaf mo:
 sequence comprising transcription (i.e.
                                                                                                                                                                                                   Pilgrim
                              polynucleotide having
                                              The invention relates
                                                                           Claim
                                                                                                    New transgenic plant, useful in developing improved characteristics or traits.
                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                     Pineda
                                                                                                                                                                                                                                                                                          (DUBE/)
(RATC/)
                                                                                                                                                                                                                                                                                                                                 (PILG/)
                                                                                                                                                                                                                                                                                                                                                                                (REUB/)
(KEDD/)
(YUGG/)
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                                                                                                                                                                                                                                                                                                                                                   (SAMA/)
                                                                                                                                                                                                                                                                                                                                                                    (JIAN)
                                                                                                                                                                                                                                                                                                                                                                                                                          (PINE/
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(FROM/)
(HEAR/)
                                                                                                                                                                                                                                                               (SHER/)
                                                                                                                                                                                                                                                                              KUMI/
                                                                                                                                                                                                                                                                                                                       CREE/
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.../) RIECHMANN J L.
.//) ADAM L J.
./) BROUN P E.
PINEDA
TOTAL
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                                                                                                                                              2004-225755/21.
DB; ADO01614.
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m ML,
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YU G.
SAMAHA R S.
PILGRIM M L.
CREELMAN R A.
DUBELL A N.
RATCLIFFE O.
KUMIMOTO R.
SHERMAN B K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZHANG J.
FROMM M
HEARD J
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Reuber TL,
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2000US-00713994.
2001US-00819142.
2001US-00837444.
2001US-00958131.
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2000US-00506720.
2000US-00532591.
2000US-00533029.
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2000US-00533392
2000US-00533648
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TL, Keddie JS, ...
va, Dubell AN,
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5-00225066.
5-00225067.
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3-0434166P.
    o o
to a transgenic plant comprises a recombinant a polynucleotide sequence or its complementary sequence encoding a polypeptide, that initiates transcription factor) from Arabidopsis, Soybean
                                                                        213pp;
                                                                        English
                                                                                                                                                                                                   Riechmann JL, Adam
S, Yu G, Jiang C,
ll AN, Ratcliffe O,
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plant size; leaf morphology;
                                                                                                                phenotypes with
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Samaha RS;
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Kumimoto R;
                                                                                                                   altered
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ID ADN73
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AC ADN7
AC ADN7
DT 15-J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -ADD03527 or ADD03530-ADD0359. Also included are using a transgenic constitutive, inducible or tissue-specific promoter and a recombinant constitutive, inducing a modified plant having a modified trait, identifying consette, producing a modified plant having a modified expression consetter that is modified plant that may be produced by the polynucleotide sequence and identifying at least one downstream conjugations are polynucleotide sequence that is subject to a regulatory effect of any of the polypeptides encoded by the polynucleotide described above. The colypeptides encoded by the polynucleotide described above. The colling germination in cold conditions freezing tolerance, tolerance to heat, tolerance to about that has an altered constitution, colerance to potassium cold conditions, freezing tolerance to be alt, tolerance to phosphate limitation, tolerance to potassium coll instation, decreased sensitivity to nitrogen limitation, altered colorance to ethylene, disease resistance, altered susceptibility to the polynucleotide susceptibility to altered s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 19
                                                                                         plant; transgenic; E2Fa/DPa transcript: animal feed product; thale cress; cell nitrogen metabolism; carbon metabolism
                                                                                                                                                                                                                                                                                                           Thale
                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADN73807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADN73807 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in root anthocyanins, increase in plant anthocyanins, and alteration light response or shade avoidance. The present sequence represents a thalecress transcription factor of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 GVRRRPWGKFAAEIRDPKK 120
                                                                                                                                                                                                                                                                                                           cress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                           protein repressed in E2Fa/Dpa expressing plants SeqID 1702
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ã,
                                                                                                                                        E2Fa/DPa transcription factor; growth regulator; t; thale cress; cell wall biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.4%; Score 19; DB
100.0%; Pred. No. 3e
tive 0; Mismatches
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Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal transduction, storage lipid mobilisation and/or altered photosynthesis, each relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a role in a variety of biological processes such as DNA replication, cell wall biosynthesis, nitrogen and/or carbon metabolism or they function as transcription factors. This polypeptide sequence is thale cress protein expressed by a gene repressed 1.3 fold or more in plants overexpressing the E2Fa/DPa transcription factor, given in an exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                characteristics. Specifically, it refers to identifying genes that are up or down-regulated in transgenic plants overexpressing the heterodimeric EZFA/DPA transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, enzymes, therappeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Altering plant characteristics, useful for producing plants for enzyme pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Altering plant pharmaceutical
                                                                               secondary; alkaloid; food colouring; flavo
                                                                                                                     AP2; transcription factor; plant
                                                                                                                                                         Plant transcription factor AP2 DNA-binding domain polypeptide
                                                                                                                                                                                                                                                                       AAY97227 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1702; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-OCT-2002; 2002EP-00079408
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                                                                    insecticide;
                                                                                                                                                                                               19-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                102 GVRRRPWGKFAAEIRDPKK 120
                                                                                                                                                                                                                                                                                                                                                              94 GVRRRPWGKFAAEIRDPKK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity 100.0%; I
19; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226
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                                                                  gene expression; modulation
                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ž
                                                                                     flavouring; fragrance; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              slates to a novel method for altering or
Specifically, it refers to identifying
                                                                                                      actor; plant metabolism; metabolite; primary;
terpenoid indole alkaloid; TIA; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                    %; Score 19; DB
%; Pred. No. 3e-
0; Mismatches
                                                                                                                                                                                                                                                                       210 AA
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3e-09;
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                                                                                                                                                                                                                       Many plant secondary metabolites have value as pharmaceuticals, food colourings, flavours and fragrances. Some plant secondary metabolites are clinked to plant or plant cell defence mechanisms and may confer to the plant antimicrobial activity, protection against UN light, herbivores, compatible indole alkaloids (TIA) represent a class of pharmaceutically cuseful compounds which maturally occur in many plant species. New methods are described which medulate the expression of one or more genes involved in the biosynthesis of plant metabolites or their precursors in plant cells. The method comprises inserting into a plant cell a sequence encoding a transcription factor comprising an AP2 DNA-binding domain and comprising an AP2 DNA-binding domain are useful as central cregulators of complex metabolite pathways involving numerous target genes for such transcription factors. This means that the yield of commercially containable metabolite compounds can be enhanced and the tolerance of plants commarcially the level of one or more metabolite is enhanced towards exogenous stress factors can be influenced. The method is useful compounds exogenous stress factors can be influenced. The method is useful towards exogenous stress factors can be influenced. The method is useful to which the transcription factor to the cell the level of the metabolite is enhanced by at least 10%, 25% or 100% or reduced 10%, 25%, 50% or 90% relative to
                                                                                Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modulating level of metabolites and stress resistance in recombinant cells for synthesis of plant metabolites such as alkaloids including trapscription factor to the
                                                                                                                                                                   Sequence 210 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 97; 101pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-FEB-1999;
10-FEB-1999;
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                                                                                                                                                                                                               cell to which the transcription factor is not provided
                     102 GVRRRPWGKFAAEIRDPK 119
129 GVRRPWGKFAAEIRDPK 146
                                                                                l Similarity
18; Conserv
                                                                              8.9%; Score 18; DB 3; Le ilarity 100.0%; Pred. No. 2.4e-08; Conservative 0; Mismatches 0;
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99US-0119388P.
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                                                                                                                       Length 210;
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                                                                                  Gaps
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5. j

Search completed: February 27, 2005, 22:23:23 Job time : 166 secs

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GenCore version 5.1.6 Copyright (c) 1933 - 2005 Compugen Ltd.  in search, using sw model  bruary 27, 2005, 22:18:21, Search time 43 Seconds 3 SERIISVEDRELLSLIEBH
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Sequence 9, Application US/09300672

Ratent No. 6248937

GENERAL INFORMATION:

APPLICANT: Finkelstein, Ruth R.

APPLICANT: Lynch, Tim

APPLICANT: Goodman, Howard M.

APPLICANT: Wang, Ming-Li

TITLE OF INVENTION: A TRANSCRIPTION FACTOR REGULATING SEED DEVELOPMENT,

TITLE OF INVENTION: QUALITY AND COLD-TOLERANCE

FILE REFERENCE: 480.89 (HV)

CURRENT APPLICATION NUMBER: US/09/300,672

4 4 5	43	42	41	40	39	38	37	36	35	34	ω u	32	31	30	29	28
10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
4. 9.	. 4	4.9		4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9
408	379	379	367	349	291	289	273	266	258	256	249	246	203	203	175	153
.a. u	40	4	w	w	4	4	4	4.	4	4	4	w	4	4	4	4
US-08-213-4198-19	US-09-270-767-49230	US-09-270-767-34013	US-08-213-419B-15	US-09-162-524-3	US-09-248-796A-14273	US-09-270-767-60136	US-09-248-796A-25975	US-09-248-796A-14280	US-09-485-529-20	US-09-485-529-5	US-09-248-796A-27128	US-09-185-160-7	US-09-270-767-50543	US-09-270-767-35326	US-09-248-796A-23457	US-09-248-796A-28015
Sequence 19, Appl	4.9	Sequence 34013, A	15	Sequence 3, Appl	Sequence 14273,	Sequence 60136,	Sequence 25975,	14	Sequence 20, Appl	Sequence 5, Appl	Sequence 27128,	Sequence 7, Appl	Sequence 50543,	Sequence 35326,	Sequence 23457,	Sequence 28015,

## ALIGNMENTS

RESULT 1 US-09-300-672-9

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Query Match
Best Local Similarity 100.0%; Pred. No. 9e-09;
Matches 17; Conservative 0; Mismatches 0; Gaps 0;

Qy 102 GVRRRPWGKFAAEIRDP 118

| | | | | | | | | | | | | | | | | |
| Db 3 GVRRRPWGKFAAEIRDP 19

RESULT 2
US-08-912-272-17
i Sequence 17, Application US/08912272
; Patent No. 6093874
; GENERAL INFORMATION:
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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OPERATING SYSTEM:

PC-DOS/MS-DOS

Release #1.0, Version #1.30

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US-09-026-039-17
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                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/090: Sequence 17, Application US/090: Patent No. 6329567
GENERAL INFORMATION: Joshkur, K. Diane APPLICANT: Okamuro, Jack K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/026,039
                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
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FILING DATE: 20-UUN.1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/700,152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 15-AUG-
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 20-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                           APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Region LOCATION: 36..51 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Peptide LOCATION: 1..69 OTHER INFORMATION: OTHER INFORMATION:
FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 8.4%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 GVRRRPWGKFAAEIRDP 118
                                                                                                                                                                 94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVRRRPWGKFAAEIRDP 22
                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09026039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 amino acids
                                                                                                                                                                                      USA
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                    19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "putative EREBP-1 amphipathic
alpha-helix"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "AP2 domain within tobacco
EREBP-1"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      023070-067220US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
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US-09-202-161B-25
                                                                                                                   US-09-202-161B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-026-039-17
                                                                                                                                                 SEQ ID NO 25
LENGTH: 59
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 17
                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US97/10382
PRIOR FILING DATE: 1997-06-12
PRIOR APPLICATION NUMBER: 60/046,494
PRIOR FILING DATE: 1997-05-14
PRIOR APPLICATION NUMBER: 60/019,633
PRIOR FILING DATE: 1996-06-12
                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 7024-371
CURRENT APPLICATION NUMBER: US/09/202,161B
CURRENT FILING DATE: 1999-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-030 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                   SOFTWARE: ASCII
                                                                                                                                                                                                                  PRIOR FILING DATE: 1996-06-12
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Purdue Research Foundation
TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
                                                                                                                                ORGANISM: Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 20-JUN-1997 PRIOR APPLICATION DATA:
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FILING DATE: 15-AUG-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 20-AUG-1996 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 GVRRRPWGKFAAEIRDP 118
106 RPWGKFAABIRDP 118
                                                                                                                                                                                                                                                                                                                                                                                                                              25, Application US/09202161B
                                            cn 6.4%; Score 13; DB 4;
1 Similarity 100.0%; Pred. No. 5.9e-0
13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 GVRRRPWGKFAAEIRDP 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 amino acids
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(415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.4%;
100.0%; Pr
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alpha-helix"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "AP2 domain within tobacco
EREBP-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17; pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
1e-08;
                                                                   5.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 69
                                                                                   Length 59;
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                                                    Indels
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                                                 Gaps
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RPWGKFAAEIRDP 20

RESULT 5 US-08-949-603-11

Application US/08949603

Patent No.

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IELEX: NO. 5891859e
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 61
TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/706,270

FILLING DATE: September 4, 1996

ATTORNEY/AGENT INFORMATION:

NAME: IAN C. MCLeod

REGISTRATION NUMBER: 0,931

REFERENCE/DOCKET NUMBER: MSU 4.1-384

TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 347-4100

TELEPAX: (517) 347-4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Michael F. Thomashow and
APPLICANT: Eric J. Stockinger
                                                                                                                                                                                                                                                                                            MOLECULE NO HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: I
                                                                                                                                                                                                                                                                ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS 5.00
SOFTWARE: Wordporfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
MEDIUM TYPE: storage
PUBLICATION INFORMATION:
                                                                                       POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
                                                                                                          MMEDIATE SOURCE:
                                                                                                                                                                    INDIVIDUAL ISOLATE: N
DEVELOPMENTAL STAGE:
HAPLOTYPE: N/A
TISSUE TYPE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Comp
OPERATING SYSTEM:
           LOCATION:
IDENTIFICATION METHOD: sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                       ORGANELLE:
                                                                                                                                      CELL TYPE:
                                                                                                                                                                                                                                              ORGANISM: Tobacco
                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: Lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Okemos
STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2190 Commons Parkway
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                                                                                                                                                                                                                                                                                                                                               Linear
                                                                                                                                                        N/A
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                                                                                                                                                                                                                                                                                                                              Polypeptide
                                                                                                                                                                                                                                                                                                                                                            Single
                                                                                        N/A
E: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA AND ENCODED PROTEIN WHICH REGULATES COLD AND DEHYDRATION REGULATED GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/949,603
                             sequencing
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Query Match

6.4%;

Score 13;

DB 2;

Length 61;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0%; Pred. No. 6.1e-05; Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                           TELEX: No. 5892009e
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Michael F
APPLICANT: Eric J. S
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                  FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS 5.00
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,
                                                                                                                                                                                                                                                                         MOLECULE TYPE: PO
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: Septemb
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                          FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEPAX: (517) 347-4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                               ORGANELLE: N/I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
                                                              OSITION IN GENOME:
                                                                                                            CELL TYPE:
                                                                                                                                           DEVELOPMENTAL STAGE:
HAPLOTYPE: N/A
TISSUE TYPE: N/A
                                                                                                                                                                                        STRAIN:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Okemos
STATE: Michia
                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: Sir
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                        TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb MEDIUM TYPE: storage
                                                                                                                                                                                                                          ORGANISM: Tobacco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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[DENTIFICATION METHOD: sequencing
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                                                                                                                                                                                                                                                                                                             Polypeptide
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DNA AND ENCODED PROTEIN
WHICH REGULATES COLD AND
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US-08-949-580-11
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Patent No. 5929305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.4%; Sc
Best Local Similarity 100.0%; F
Conservative 0;
                                                                                                                                                                                                                                                                                                                 NAME: Ian C. McLecu
NAME: 1an C. McLecu
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-383
TELECOMYUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
                                                                                                                                                                                                                                                                                                           TELEX: NO. 5929305e INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                 TOPOLOGY: Linear MOLECULE TYPE: Pol HYPOTHETICAL: No ANTI-SENSE: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS-DOS 5.00
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                     DEVELOPMENTAL STAGE
HAPLOTYPE: N/A
HAPLOTYPE: N/A
                                                                                                                                                     FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: September 4, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Michael APPLICANT: Eric J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
              CELL TYPE:
CELL LINE:
ORGANELLE:
                                                                                                                                                                                                                               TYPE: Amino Acid
STRANDEDNESS: Sir
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette, 5.25 inch, 360 MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                    ORGANISM: Tobacco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                        INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 RPWGKFAAEIRDP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 RPWGKFAAEIRDP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okemos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Michigan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2190 Commons Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eric J. Stockinger
VENTION: DNA AND ENCODED PROTEIN
VENTION: WHICH REGULATES COLD AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ian C.
                                                                                          STAGE:
                                                                                                                                                                                                                 Polypeptide
                                                                                                                                                                                                                                              Single
N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F. Thomashow and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McLeod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEHYDRATION REGULATED GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08/706,270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/949,580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.1e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/949,580
FILING DATE: October 14, 1997
APPLICATION NUMBER: 08/706,270
FILING DATE: September 4, 1996
ATTORNEY/AGENT IMFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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MEDIUM TYPE: Diskette, 5
MEDIUM TYPE: Storage
MEDIUM:

                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: NO. 5965705e INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                          MOLECULE TYPE: PO
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 10/14/1997
CLASSIFICATION:
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OTHER INFORMATION: Figure
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (517) 347-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Michael F. Thomashow and APPLICANT: Eric J. Stockinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POSITION IN GENOME:
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                                                                                                                                                                                                                                                                                                                                          TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
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INDIVIDUAL ISOLATE: N/A
                                                          ORGANISM: Tobacco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.0%; Ees 13; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T: 2190 Commons Parkway
Okemos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (517) 347-4103
                                                                                                                                                                                                                                                                            Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
NYSTEM: MS-DOS 5.00
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                                                                                                                                                                                                                                           Polypeptide
                                                                                                                                                                                                                                                                                                             Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA AND ENCODED PROTEIN WHICH REGULATES COLD AND DEHYDRATION REGULATED GENES
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ire 2D
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DEVELOPMENTAL ST HAPLOTYPE: N/A TISSUE TYPE: N/

N/A

CELL TYPE:

N/A

STAGE: /A N/A

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RESULT 10
US-09-601-802D-11
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                                                                                                                                 Query Match
Best Local (
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Best Local Similarity 100.0%; Pred. No. 6.1e-05;
                                                                                                                   Matches
                                                                                                                                                                                                                                     SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Appli
Patent No. 6417428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Plant Having Altered Environmental Stress Tolerance FILE REFERENCE: 19117.713 Seq List CURRENT APPLICATION NUMBER: US/09/198,119C CURRENT FILING DATE: 1998-11-23
                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jiang, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: Figure PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-0
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                                                                                                                                                                                        TYPE: PRT ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                    LENGTH: 61
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL LINE:
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US FILING DATE: 1998-02-03
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                                                                                      106 RPWCKFAAEIRDP 118
                                                                                                                  l Similarity
13; Conserv
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                                                          RPWGKFAAEIRDP 20
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Jiang, Cai-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jaglo-Ottosen, Kirsten
Gilmour, Sarah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stockinger, Eric
                                                                                                                   Conservative
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1998-09-04
                                                                                                                                                                                                                                                                                                               1998-02-03
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1998-02-03
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2.0
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                                                                                                                                 Score 13; DB 4; 
; Pred. No. 6.1e-0
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                                                                                                                   Mismatches
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                                                                                                                                            Length 61;
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CURRENT APPLICATION NUMBER: US/09/601,802D
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/018,233
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: 09/017,816
PRIOR APPLICATION NUMBER: 09/018,235
PRIOR APPLICATION NUMBER: 09/018,235
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR PILING DATE: 1998-02-03
PRIOR PILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03

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APPLICANT: Jiang, Cai-Zhong
APPLICANT: Liang, James
APPLICANT: Liang, James
APPLICANT: Haake, Volker
APPLICANT: Haake, Volker
TITLE OF INVENTION: PLANT HAVING ALTERED ENVIRONMENTAL
TITLE OF INVENTION: STRESS TOLERANCE
FILE REFERENCE: 51444200201/MEJ0029
CURRENT APPLICATION UNMERR: US/09/601,802D
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/018,233
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: 09/018,235
PRIOR APPLICATION NUMBER: 09/018,235
PRIOR APPLICATION NUMBER: 09/018,235
PRIOR APPLICATION NUMBER: 09/018,237
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Best Local Similarity
Matches 13; Conserve
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LENGTH: 61
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                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                   APPLICANT:
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Zhang, James
APPLICANT: Hang, James
APPLICANT: Haske, Volker
TITLE OF INVENTION: PLANT HAVING ALTERED ENVIRONMENTAL
TITLE OF INVENTION: STRESS TOLERANCE
FILE REFERENCE: 514442000201/MBI0029
                                                                                                                                                                                      APPLICANT: Thomashow, Michael APPLICANT: Stockinger, Eric APPLICANT: Jaglo-Ottosen, KiAPPLICANT: Gilmour, Sarah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thomáshow, Michael APPLICANT: Stockinger, Eric APPLICANT: Jaglo-Ottosen, KiAPPLICANT: Gilmour, Sarah APPLICANT: Zarka, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/198,119 PRIOR FILING DATE: 1998-11-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/018,234
PRIOR FILING DATE: 1998-02-03
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                                                                                                                                                                                      Stockinger, Eric
Jaglo-Ottosen, Kirsten
Gilmour, Sarah
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Gilmour, Sarah
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                                                                                                                                                           Zarka, Daniel
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100.0%; Pr
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Pred. No.
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US-08-912-272-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/198,119 PRIOR FILING DATE: 1998-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/700,152 FILING DATE: 20-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/879,827
FILING DATE: 20-JUN-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Line CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity hes 13; Conserv
                                                                                                                                                                                                                                                        NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-067220US
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 15-AUG-1997 CLASSIFICATION: 800
                                                                                                     TOPOLOGY:
                              NAME/KEY: Peptide
LOCATION: 1..69
                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                      LENGTH:
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FILING DATE: 1998-02-03
APPLICATION NUMBER: 09/018,234
FILING DATE: 1998-02-03
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 INFORMATION:
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                                                                                                                                  amino acids
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/note= "AP2 domain within tobacco
EREBP-2"
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ches 0;
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Best Local Simi
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Patent No. 6093874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/879,827
FILING DATE: 20-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/700,152
FILING DATE: 20-AUG-1996
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRE
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APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
TITLE OF INVENTION: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
LOCATION: 35..51
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                  NAME/KEY:
                                                                                                                                                                  OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                               NAME/KEY: Peptide LOCATION: 1..69
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                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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13; Conservative
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35..51
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100.0%; PI
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100.0%; Pred. No. 6.1
ive 0; Mismatches
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alpha-helix"
   /note= "putative EREBP-4 amphipathic
alpha-helix"
                                                                                                                                                                     /note= "AP2 domain
EREBP-4"
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                                                                                                                                                                                                       within tobacco
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US-09-026-039-18
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                 Query Match
Best Local S
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Best Local
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/879,827
FILING DATE: 20-JUN-1997
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/912,272
FILING DATE: 15-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: methods
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/700,152 FILING DATE: 20-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                  NAME/KEY: Region
LOCATION: 35..51
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                   NAME/KEY: Peptide LOCATION: 1..69 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/026,039 FILING DATE: 19-FEB-1998
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                                                                                                                                                                                                                                                                                                                             ENGTH:
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                   Similarity
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                                                                                                                                                                                                                                                                                                                           69 amino acids
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Conservative 0; Mismatches
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100.0%; Pred. No. 6.8e-05;
                   6.4%; Score 13; DB 3; L
L00.0%; Pred. No. 6.8e-05;
                                                                                  /note= "putative EREBP-2 amphipathic
alpha-helix"
                                                                                                                                                                     /note= "AP2 domain within tobacco
EREBP-2"
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                                   Length 69;
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                                                                    Matches
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Best Local (
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Patent No. 6329567
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 15-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 20-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 15-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPEKALLING PATENTIN Release #1..,
SOFTWARE: PatentIn Release #1..,
CURRENT APPLICATION DATA:
US/09/026,039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: IWO CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 20-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                    NAME/KEY: Region LOCATION: 35..51 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                     LOCATION: 1..69
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111-3834
                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                 106 RPWGKFAAEIRDP 118
 10 RPWGKFAAEIRDP 22
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                                                                                  Similarity
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                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                  6.4%;
                                                                                                                                                /note= "putative EREBP-4 amphipathic
alpha-helix"
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EREBP-4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 08/700,152
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                                                                 s; Score 13; DB; Pred. No. 6.8
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                                                           DB 3; bc. 3. 6.8e-05; 0;
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Gaps

Search completed: February 27, 2005, 22:27:58 Job time : 44 secs

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Title:
Perfect score:
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
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                                                         Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

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                                                                                                                                                                                                               / Cgn12 6/ptodata/1/pubpaa/US09A PUBCOMB.pep: *
/ Cgn2 6/ptodata/1/pubpaa/US09A PUBCOMB.pep: *
/ Cgn2 6/ptodata/1/pubpaa/US09A PUBCOMB.pep: *
/ Cgn2 6/ptodata/1/pubpaa/US09C PUBCOMB.pep: *
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/ Cgn2 6/ptodata/1/pubpaa/US10C PUBCOMB.pep: *
/ Cgn2 6/ptodata/1/pubpaa/US10D PUBCOMB.pep: *
/ Cgn2 6/ptodata/1/pubpaa/US10 NEW PUB.pep: *
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SUMMARIES
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PUBCOMB.pep:*
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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
1	23	11.3	137	15	US-10-425-114-52229	Sequence 52229, A
Ŋ	23	11.3	146	15	US-10-424-599-214399	
ω	23	11.3	199	15	US-10-424-599-214365	
4.	23	11.3	203	15	US-10-425-114-36689	Sequence 36689, A
ຫ	19	9.4	156	15	US-10-424-599-208822	
σ	19	9.4	202	15	US-10-424-599-175489	
7	19	9.4	226	15	US-10-225-068-128	Sequence 128, App
æ	19	9.4	226	15	US-10-374-780A-6	Sequence 6, Appli
9	19	9.4	226	15	US-10-412-699B-28	Sequence 28, Appl
10	17	8.4	124	15	US-10-374-780A-1737	Sequence 1737, Ap
11	17	8.4	139	10	US-09-934-455-6	Sequence 6, Appli
12	17	8.4	139	15	US-10-225-068-46	Sequence 46, Appl
13	17	8.4	139	15	US-10-225-066A-170	Sequence 170, App

RESULT 2 US-10-424-599-214399

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234	220	219	218	218	218	218	218	218	167	150	131	131	112	1040	299	299	299	282	224	222	214	209	207	207	201	201	201	201	178	152	139
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US-10-424-599-160662	0-425-114-	-10-424	US-10-412-699B-800	US-10-374-780A-252	US-10-225-067-70	US-10-225-066A-58	US-10-225-068-210	9-9	US-10-424-599-149169	US-10-424-599-223956	US-10-374-780A-1736	0	US-10-424-599-247090	US-10-437-963-120630	US-10-437-963-156010	US-10-412-699B-1360	US-10-374-780A-1157	US-10-374-780A-503	US-10-425-114-41699	-425-114	425	US-10-424-599-173483	-41	0-278-	0-412-	0-412-	US-10-374-780A-2230	US-10-225-066A-788	0-424	0-425-114-	US-10-374-780A-332
Sequence 16066	Sequence 40926	Sequence 15483	Sequence 800,	e 252,	e 70,	e 58,	e 210	e 192	æ		ø		Sequence 247090		Sequence 156010	Sequence 1360		Sequence 503,	æ	Œ		173	54,	e 54,	e 172	e 50,	e 223	e 788,	æ	e 41	Sequence 332,
562,	26, A	332,		App	App1	Appl	, App	App	169,	956,	5, Ap	, App	390,	530,	010,		7, Ap		•	20, A	•	183,	App1	App1	s, Ap	App1	), Ap	App	305,	31, A	App

## ALIGNMENTS

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; OTHER INFORMATION: Clone ID: 700869231_FLI.pep
US-10-425-114-52229
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                                                                                                                                                                                                                                              APPLICANY: Screen, Steven E
APPLICANY: Tabaska, Jack E
APPLICANY: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 52229
LENGTH: 137
TYPE: PRT
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Davi
                                                                                        Query Match 11.3%; Score 23; DB 15; Best Local Similarity 100.0%; Pred. No. 7.4e-13; Matches 23; Conservative 0; Mismatches 0;
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Publication No. US20040034888A1
Zhou, Yihua
Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David
APPLICANT: Screen, Steven
APPLICANT: Tabaska, Jack
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 213365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-2318

FILE REFERENCE: 38-21(53223)B
                                                                                                                    Sequence 36689, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
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SEQ ID NO 214399
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CURRENT FILING DATE: 2003-04-28
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Clone ID: PAT_MRT3847_3559C.1.pep
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Similarity 100.0%;
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                    Kovalic, David K
Screen, Steven E
Tabaska, Jack E
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100.0%; Pr
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SEQ ID NO 36689

LENGTH: 203
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 208822
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 175489
LENGTH: 202
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
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ORGANISM: Glycine max
FEATURE:
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ORGANISM: Glycine max
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; Pred. No.
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1e-12;
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RESULT 8
US-10-374-780A-6
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; LCCATION: (89)...(157)
; OTHER INFORMATION: Conserved domain
US-10-225-068-128
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             Sequence 6, Application US/10374780A
Publication No. US20040019927A1
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-12-11
PRIOR FILING DATE: 2001-12-11
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 128
LENGTH: 226
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Best Local :
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Publication No. US20030217383A1
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yu, Guo-Liang
APPLICANT: Broun, Pierre E.
TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES
TITLE OF INVENTION: POLYBEPTIDES IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/225,068
CURRENT FILING DATE: 2002-08-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 514442002040
   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Glycine
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                                                                                                                                                                                                                                                         Local Similarity
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al Similarity 100.0%;
19; Conservative
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Riechmann, Jose Luis
Heard, Jacqueline E.
Jiang, Cai-Zhong
Adam, Luc J.
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Riechmann, Jose Luis
Jiang, Cai-Zhong
Heard, Jacqueline E
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                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                     9.4%; Score 19;
100.0%; Pred. No.
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Pred. No. 4.6e-09;
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APPLICANT:
APPLICANT:
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                         Yu, Guo-Liang
Jiang, Cai-Zhong
Samaha, Raymond R.
Pilgrim, Marsha L.
                                                                                      Pineda, Omaira
Reuber, T. Lynne
Keddie, James S.
                                                                                                                                                    Riechmann, J. Adam, Luc J.
                                                                                                                                                                                  Zhang, James
Fromm, Michael E.
Heard, Jacqueline
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o. US20040045049A1
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                                                                                                          Lynne
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; OTHER INFORMATION: G22
US-10-374-780A-6
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CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION UNMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION UNMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION UNMBER: 09/934,455
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 2001-08-22
                                                                                                                                                                                                                           SEQ ID NO 6
LENGTH: 226
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
                                                                                                             Query Match 9.4%; Score 19; Best Local Similarity 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 10/225,068
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PatentIn version 3.2
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PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
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PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 10/225,066
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
FILE REFERENCE: MBI-0047 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2002-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 10/225,067 FILING DATE: 2002-08-09
                            102 GVRRRPWGKFAAEIRDPKK 120
94 GVRRRPWGKFAAEIRDPKK 112
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Keddie, James
Broun, Pierre E
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Dubell III, Arnold T
Pineda, Omaira
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                                                                                        Conservative
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                                                                                          Mismatches
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; OTHER INFORMATION: G22
US-10-412-699B-28
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NUMBER OF SEQ ID NOS: 2011
SOFTWARE: PatentIn version 3.2
SEQ ID NO 28
LENGTH: 226
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Best Local Similarity 100.0%;
Matches 19; Conservative (
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APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
FILE REFERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
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APPLICANT: Riechmann, Jose Luis
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PRIOR FILING DATE: 2001-03-27
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PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,392
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TLE OF INVENTION: Polynucleotides and Polypeptides in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/532,591
FILING DATE: 2000-03-22
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APPLICATION NUMBER: 09/533,029
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Adam, Luc J
Reuber, T. Lynne
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Haake, Volker
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Kumimoto, Roderick
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Dubell III, Arnold T
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Broun, Pierre E
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5e-09;
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Query Match
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CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR PILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: PATENTIN VETSION 3.1
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PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,067
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,068
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
SOFTWARE: Patentin version 3.2
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LENGTH: 124
TYPE: PRT
ORGANISM: Oryza sativa japonica
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                                                                                                                                                                                SEQ ID NO 6
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Best Local
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PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
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PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR FILING DATE: 2001-08-22
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PRIOR APPLICATION NUMBER: 60/338,692
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                                                                                                                TYPE: PRT
ORGANISM: Arabidopsis thaliana
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                                                                                                                                                           ENGTH: 139
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INVENTION: Genes for Modifying Plant Traits
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Ratcliffe, Oliver
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Jiang, Cai-Zhong
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                  8.4%; Score 17; DB nilarity 100.0%; Pred. No. 2.2 Conservative 0; Mismatches
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                  DB 10; I
. 2.2e-07;
ches 0;
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102 GVRRRPWGKFAAEIRDP 118

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Matches 17; Conserve
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US-10-225-066A-170
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TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES
TITLE OF INVENTION: POLYPETTIDES IN PLANTS
                                                                                                                                                  APPLICANT: Mendel Biotechnology, Inc. APPLICANT: RATCLIFFE, Oliver
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PRIOR FILING DATE: 2001-12-11
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PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
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CURRENT FILING DATE: 2002-08-09
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OTHER INFORMATION: Conserved domain
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ORGANISM: Arabidopsis thaliana
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                       DUBELL, Arnold T
HEARD, Jacqueline E
PILGRIM, Marsha L
JIANG, Cai-Zhong
REUBER, T. Lynne
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CREELMAN, Robert A
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Pred. No.
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2.2e-07;
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CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR PRILING DATE: 2001-04-18
PRIOR PRILING DATE: 2001-08-09
PRIOR PRILING DATE: 2001-08-09
PRIOR PRILING DATE: 2001-08-09
PRIOR PRILING DATE: 2001-08-22
PRIOR PRILING DATE: 2001-11-19
PRIOR PRILING DATE: 2001-11-19
PRIOR PRILING DATE: 2001-11-19
PRIOR PRILING DATE: 2001-12-11
PRIOR PRILING DATE: 2001-12-11
PRIOR PRILING DATE: 2001-12-11
PRIOR PRILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR PRILING DATE: 2002-08-09
PRIOR PRILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR PRILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR APPLICATION NUMBER: 10/225,066
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PRIOR PRILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,066
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PRIOR FILING DATE: 2001-04-18
PRIOR PELICATION NUMBER: 60/310,847
PRIOR PELICATION NUMBER: 60/310,847
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR PILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR PILING DATE: 2001-12-11
PRIOR PILING DATE: 2001-12-11
PRIOR PILING DATE: 2001-12-11
PRIOR PILING DATE: 2002-06-14
NUMBER: OF SEQ ID NOS: 1122
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LENGTH: 139
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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ORGANISM: Arabidopsis thaliana
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Jiang, Cai-Zhong
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Dubell III, Arnold T
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Broun, Pierre E
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Haake, Volker
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100.0%; Pred. No.
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Sequence 41831, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Tabus, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 41831
LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; CREANISM: Arabidopsis thaliana
; PEATURE:
; CTHER INFORMATION: G1792 (conserved domain in aa coordinates: 17-85)
US-10-374-780A-332
Search completed: February 27, 2005, 22:38:55 Job time: 130 secs
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                                                                                                                                                                                                                                                                            ; TYPE: PRT; ORCANISM: Arabidopsis thaliana; FEATURE: FEATURE: OTHER INFORMATION: Clone ID: LIB25-065-D10_FLI.pep US-10-425-114-41831
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US-10-425-114-41831
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NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PatentIn version 3.2
SEQ ID NO 332
                                                                                                                                                                                 Query Match 8.4%; Score 17; DB 15; Length 152; Best Local Similarity 100.0%; Pred. No. 2.4e-07; Matches 17; Conservative 0; Mismatches 0; Indels
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OM protein - protein search, using sw model

Perfect score: Title: US-09-890-782-6 Run on:

February 27,

2005,

22:17:56 ; Search time 40 Seconds (without alignments)

488.300 Million cell updates/sec alignments

Sequence: MSEEIISVSDRFLLSLIEEH.....SSSSSSSSSENSGGRKKRRY 203

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

pecies: Arabidopsis thaliana (mouse-ear cress)	lternate names: hypothetical protein At2g44840	ylene-responsive transcription factor homolog T13E15.15 - Arabidopsis	409	ULT 1	
		•			
		Arabidopsis			

thaliana

R;Roccession: T00409; D84883
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Massubmitted to the EMBL Data Library, July 1997
A;Description: Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence.
A;Reference number: Z14146 C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004 C;Accession: T00409; D84883

A;Status: translated from GB/EMBL/DDBJ A; Accession: T00409

A; Molecule type: DNA A; Residues: 1-226 < ROU>

A;Cross-references: UNIPROT:022167; EMBL:AC002388; NID:g3420042; PID:g2344900

A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84883

A;Status: preliminary

A; Molecule type: DNA A; Residues: 1-226 <STO> A; Cross-references: GB: GB:AE002093; NID:g2344900; PIDN:AAC31840.1; GSPDB:GN00139

C;Genetics: A;Gene: At2

A; Map position: At2g44840; T13E15.15 osition: 2

밁 Ś Best Query Match Local 102 GVRRRPWGKFAAEIRDPKK 120 l Similarity 19; Conserv 9.4%; Score 19; DB ilarity 100.0%; Pred. No. 1. Conservative 0; Mismatches DB 2; 1.4e-10; Length 226; Indels 0 Gaps .

0

RESULT 2 T49897

transcription factor-like protein - Arabidopsis thallana
N;Alternate names: protein T2I1.290
C;Species: Arabidopsis thallana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49897
R;Bevan, M; Murphy, G; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; L
submitted to the Protein Sequence Database, April 2000

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-207 <BEV>
A;Cross-references: UNIPROT:Q9LY05; EMBL:AL163912; GSPDB:GN00063; ATSP:T211.290
A;Experimental source: cultivar Columbia; BAC clone T2I1
C;Gene: ATSP:T211.290
A;Map position: 5
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T02432
RESULT 5
T04787
hypothetical protein F10M10.180
C;Species: Arabidopsis thaliana
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T03927
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Plant Cell 7, 173-182, 1995
A;Title: Ethylene-inducible DNA binding proteins that interact with A;Reference number: Z14671; MUID:95276459; PMID:7756828
A;Accession: T02432
                                                                                                                                                                                                                                                                                                                                                                                                                 DNA binding protein S25-XP1 - common tobacco C;Species: Nicotiana tabacum (common tobacco)
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                                                                                                                                                                                                                                                                                                                 A; Reference number: Z15139
A; Accession: T03927
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A;Molecule type: mRNA
A;Residues: 1-236 <OHM>
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A;Residues: 1-277 <XUP>
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 - Arabidopsis thaliana (mouse-ear cress)
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106 RPWGKFAAEIRDP 118

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A;Access.....A;Access.....A;Access....A;Acolecule type: DNA
A;Residues: 1-268 <BEV>
A;Residues: 1-268 <BEV>
A;Cross-references: UNIPROT:Q9SZ06; EMBL:AL035521
A;Cross-references: cultivar Columbia; BAC clone F10M10
                                                                                                                                                                                R;Ohme-Takagi, M.; Shinshi, H.
Plant Cell 7, 173-182, 1995
A;Title: Ethylene-inducible DN
                                                                                                                                                                                                                                                      T02590
DNA binding protein EREBP-2 - common tobacco
DNS C:Species: Nicotiana tabacum (common tobacco)
C:Species: Nicotiana tabacum (revision 05-Maz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 402, 769-777, 1999
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EREBP-2 protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Bevan, M.; De Haan, M.; Maarse, A.C.; Grissubmitted to the Protein Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                      S
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A; Residues: 1-225 <STO>
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A; Accession: T04787
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C;Accession: T04787
                                                               A;Cross-references: UNIPROT:Q40479; EMBL:D38126; NID:g790362; PIDN:BAA07324.1; A;Experimental source: strain BY4; tissue-type leaf
                                                                                                A; Molecule type: mRNA
A; Residues: 1-233 < OHM >
                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                    A; Accession: T02590
                                                                                                                                                                  A; Reference number:
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13; Conserv
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               100.0%;
                                   6.48;
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Pred. No.
               Score 13;
Pred. No.
 Mismatches
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ase, February 1999
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9.2e-05;
               DB 2; Le
9.5e-05;
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ethylene responsive element binding factor 1 [imported] - Arabidopsis thaliana (c;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: T51988
R;Fujimoto, S.Y.; Ohta, M.; Usui, A.; Shinshi, H.; Ohme-Takagi, M.
Plant Cell 12, 393-404, 2000
A;Title: Arabidopsis ethylene responsive element binding factors act as transc: A;Reference number: Z25893
A;Accession: T51988
A;Accession: T51988
A;Accession: T51988
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A;Accession: T07686
A;Status: ¬¬¬¬'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ethylene responsive element binding factor 2 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004 C;Accession: T51989 R;Fujimoto, S:Y.; Ohta, M.; Usui, A.; Shinshi, H.; Ohme-Takagi, M. Plant Cell 12, 393-404, 2000 R;Title: Arabidopsis ethylene responsive element binding factors act as transc: A;Reference number: Z25893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:080338; C;Genetics:
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A;Status: prelimina
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A; Residues: 1-234 < ZH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcription factor Pti4 - tomato (fragment)
C;Species: Lycopersicon esculentum (tomato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999
C;Accession: T07686
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Best Local Similarity
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Best Local
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ilarity 100.0%;
Conservative
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100.0%; Pred. No. 9.5e-05;
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Pred. No.
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5. 9.9e-05;
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probable AP2 domain transcription factor [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 C;Accession: C84901
                                                                    RESULT
C84901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: Arabidopsis ethylene responsive element A;Reference number: Z25994
A;Accession: T52189
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                                                                                                                                                                                                                                                                                A;Experimental source: strain BY4; tissue-type lo C;Superfamily: Arabidopsis thaliana hypothetical
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                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q40478; EMBL:D38125; NID:g790361; PIDN:BAA07323.1; PID:g120
A;Experimental source: strain BY4; tissue-type leaf
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A; Residues: 1-281 <USU>
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Matches
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Best Local
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                                                                                                                                                                            106 RPWGKFAABIRDP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 RPWGKFAAEIRDP 118
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13; Conserv
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                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M.; Shinshi, H.; Ohme-Takagi, M.
EMBL Data Library, April 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNIPROT:080387; EMBL:AB013301; PIDN:BAA31525.1
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100.0%; Py
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                          DNA binding proteins that interact MUID:95276459; PMID:7756828
                                                                                                                                                                                                           Score 13; DB; Pred. No. 0.0
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Pred. No.
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                #text_change 09-Jul-2004
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Causs, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Causs, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Causs, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.M.; 
                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residus: 1-315 < DEH>
A;Cross-references: UNIPROT:Q9M374; EMBL:AL132959
A;Experimental source: cultivar Columbia; BAC clone F15G16
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A;Molecule type: mRNA
A;Residues: 1-300 <FUJ>
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A;Map position: 2
C;Superfamily: Ar:
A;Map position: 3
A;Note: F15G16.20
C;Superfamily: Arabidopsis thaliana hypothetical protein F15G16.20
                                                                                                                                                                                                                                                                                                                                                                                                                                  R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet submitted to the Protein Sequence Database, January 2000 A;Reference number: Z24480 A;Accession: T47955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F15G16.20 - Arabidopsis thaliana (C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47955
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C; Genetics:
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A; Accession: T52020
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Plant Cell 12, 393-404, 2000
A;Title: Arabidopsis ethylene responsive element binding factors act as transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ethylene responsive element binding factor 5 [validated] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
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A; Residues: 1-294 <STO>
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Best Local Similarity
Matches 13; Conserv
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rences: UNIPROT:080341; EMBL:AB008107; PIDN:BAA32422.1
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Search completed: February 27, 2005, 22:27:10
Job time : 41 secs